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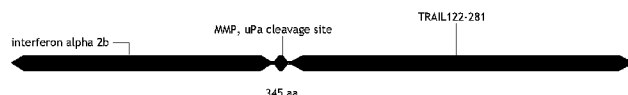
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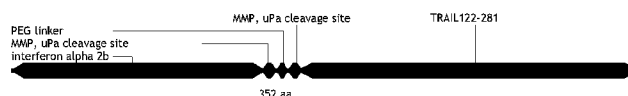
(54) **Titre: ANTICANCER FUSION PROTEIN**



Ex. 1



Ex.2



Ex. 3



Ex.4

(57) **Abrégé/Abstract:**

A fusion protein comprising domain (a) which is a functional fragment of hTRAIL protein sequence, which fragment begins with an amino acid at a position not lower than hTRAIL95, or a homolog of said functional fragment having at least 70% sequence identity; and domain (b) which is a sequence of an immunostimulating effector peptide, wherein the sequence of domain (b) is attached at the C-terminus or N-terminus of domain (a). The fusion protein can be used for the treatment of cancer diseases.

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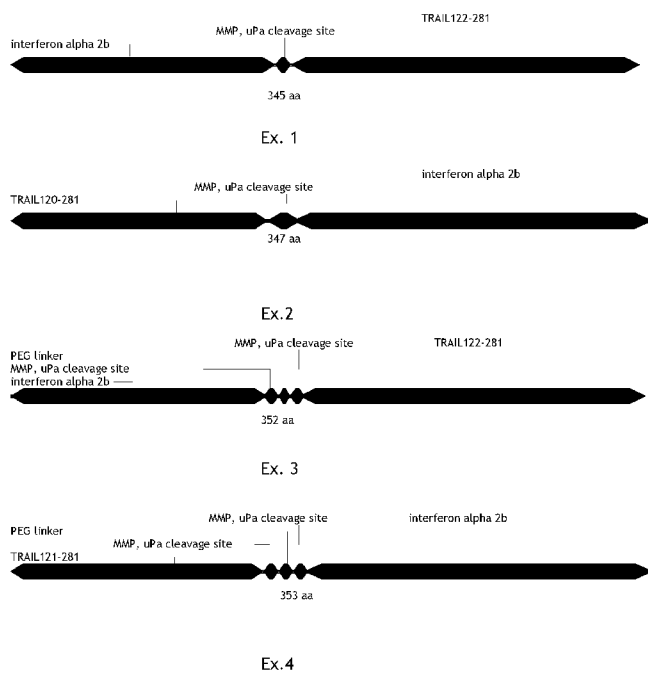


Fig. 1

(57) Abstract: A fusion protein comprising domain (a) which is a functional fragment of hTRAIL protein sequence, which fragment begins with an amino acid at a position not lower than hTRAIL95, or a homolog of said functional fragment having at least 70% sequence identity; and domain (b) which is a sequence of an immunostimulating effector peptide, wherein the sequence of domain (b) is attached at the C-terminus or N-terminus of domain (a). The fusion protein can be used for the treatment of cancer diseases.

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ANTICANCER FUSION PROTEIN

The invention relates to the field of therapeutic fusion proteins, in particular recombinant fusion proteins. More particularly, the invention relates to fusion proteins containing the fragment of a sequence of the soluble human TRAIL 5 protein in combination with a sequence of an immunostimulating peptide, pharmaceutical compositions containing them, their use in therapy, particularly as anticancer agents, and to polynucleotide sequences encoding the fusion proteins, expression vectors containing the polynucleotide sequences, and host cells containing these expression vectors.

10 TRAIL protein belonging to the cytokines family (Tumor Necrosis Factor- Related Apoptosis Inducing Ligand), also known as Apo2L (Apo2-ligand), is a potent activator of apoptosis in tumor cells and in cells infected by viruses. TRAIL is a ligand naturally occurring in the body. TRAIL protein, its amino acid sequence, coding DNA sequences and protein expression systems were disclosed for the 15 first time in EP0835305A1.

TRAIL protein exerts its anticancer activity by binding to pro-apoptotic TRAIL surface receptors 1 and 2 (TRAIL-R1/R2) and subsequent activation of these receptors. These receptors, also known as DR4 and DR5 (death receptor 4 and death receptor 5), belong to the TNF receptor family and are overexpressed by 20 different types of cancer cells. Activation of these receptors can induce external signaling pathway of apoptosis independent from suppressor gene p53, which by activated caspase-8 leads to the activation of executive caspases and thereby degradation of nucleic acids. Caspase-8 released upon TRAIL activation may also cause the release of Bid protein and thereby indirect activation of mitochondrial 25 pathway, Bid protein being translocated to mitochondria, where it stimulates the release of cytochrome c, thus indirectly amplifying the apoptotic signal from death receptors.

TRAIL acts selectively on tumor cells essentially without inducing apoptosis in healthy cells which are resistant to this protein. Therefore, the enormous poten- 30 tial of TRAIL was recognized as an anticancer agent which acts on a wide range of different types of tumor cells, including hematologic malignancies and solid tumors, while sparing normal cells and exerting potentially relatively small side effects.

TRAIL protein is a type II membrane protein having the length of 281 amino

acids, and its extracellular region comprising amino acid residues 114-281 upon cleavage by proteases forms soluble sTRAIL molecule of 20 kDa size, which is also biologically active. Both forms TRAIL and sTRAIL are capable of triggering apoptosis via interaction with TRAIL receptors present on target cells. Strong
5 antitumor activity and very low systemic toxicity of soluble part of TRAIL molecule was demonstrated using cell lines tests.

Human clinical studies with recombinant human soluble TRAIL (rhTRAIL) having amino acid sequence corresponding to amino acids 114-281 of hTRAIL, known under the INN dulanermin, showed also its good tolerance and absence of dose
10 limiting toxicity.

Fragment of TRAIL shorter than 114-281 was also found to be able to bind with membrane death receptors and induce apoptosis via these receptors, as recently reported for recombinant circularly permuted mutant of 122-281hTRAIL, for example in EP 1 688 498.

15 Toxic effects of recombinant TRAIL protein on liver cells reported up to now appeared to be associated with the presence of modification, i.e. polyhistidine tags, while untagged TRAIL showed no systemic toxicity.

However, in the course of further research and development it appeared that many cancer cells also showed primary or acquired resistance to TRAIL (see for
20 example WO2007/022214). Although the mechanism of resistance to TRAIL has not been fully understood, it is believed that it may manifest itself at different levels of TRAIL-induced apoptosis pathway, ranging from the level of cell surface receptors to the executive caspases within the signaling pathway. This resistance limits the usefulness of TRAIL as an anticancer agent.

25 Furthermore, in clinical trials on patients the actual effectiveness of TRAIL as a monotherapy proved to be low. To overcome this low efficiency and the resistance of tumors to TRAIL, various combination therapies with radio- and chemotherapeutic agents were designed, which resulted in synergistic apoptotic effect (WO2009/002947; A. Almasan and A. Ashkenazi, Cytokine Growth Factor Reviews
30 14 (2003) 337-348; RK Srivastava, Neoplasia, Vol 3, No 6, 2001, 535-546, Soria JC et al., J. Clin. Oncology, Vol 28, No 9 (2010), p. 1527-1533). The use of rhTRAIL for cancer treatment in combination with selected conventional chemotherapeutic agents (paclitaxel, carboplatin) and monoclonal anti-VEGF antibodies are described in WO2009/140469. However, such a combination necessarily implies
35 well-known deficiencies of conventional chemotherapy or radiotherapy.

Constructed fusion protein containing sequences of angiogenesis inhibitor vasostatin and TRAIL linked with a metalloprotease cleavage site linker was described as exhibiting apoptosis-inducing effect in tumor cells by A.I. Guo et al in Chinese Journal of Biochemistry and Molecular Biology 2008, vol. 24(10), 925-930. Constructed fusion protein containing sequences Tumstatin183-230 of angiogenesis inhibitor tumstatin and TRAIL114-281 was described as exhibiting induction of apoptosis of pancreatic cancer cells by N.Ren et al in Academic Journal of Second Military Medical University 2008, vol. 28(5), 676-478.

US2005/244370 and corresponding WO2004/035794 disclose the construct of TRAIL95-281 as an effector domain linked by a peptide linker with extracellular part of another member of TNF family ligands CD40 as a cell surface binding domain. It is stated that activation of the construct is via binding of its CD40 part.

Moreover, the problem connected with TRAIL therapy has proved to be its low stability and rapid elimination from the body after administration.

Advantageous effect of cytokines in cancer therapy is also known. A member of the cytokines family is interferon, a protein that stimulates the immune system. Interferons are important anti-cancer agents or adjuncts anti-cancer therapeutics (Borden and Williams, Interferons, Cancer Medicine, 5th edition, 815-824, 2000). It has been shown that one of the effects of interferons is strong stimulation of multiple proapoptotic factors, including TRAIL ligand.

A representative of Type II inteferons group is interferon gamma (IFN- γ) which is a dimeric soluble cytokine. IFN- γ is secreted by NK, NKT, Th1, Tc, and dendritic cells. IFN- γ ligand binds to two types of IFN- γ receptor R α and IFN- γ RB1 and activates the JAK-STAT pathway. One of its effects is the intense stimulation of human monocytes to produce TRAIL protein, which significantly affects their ability to eliminate cancer cells (Griffith et al, J. Exp. Med., 189:1343-1353, 1999).

Interferon gamma activates IFN gamma receptor, stimulating antibody-dependent toxicity and potentiates the process of connecting the cells with tumor cells. In addition, IFN gamma activates caspases, thereby inducing apoptosis in cancer cells. In addition, it has been demonstrated that in many tumor lines showing resistance to TRAIL-stimulated apoptosis interferon gamma acted synergistically, contributing to their sensitivity to TRAIL (Wang et al,

Oncogene, 23: 928-935, 2004). However, existing therapies using IFN gamma were not sufficiently effective to find use in the treatment of cancer diseases.

Beneficial effects of interferon alpha on the induction of overproduction of TRAIL in myeloma, lymphomas and liver cancer cells has been also demonstrated
5 (Chen and et al, Blood, 98: 2183-21192; Herzer et al, Cancer Res. 69(3): 855-862, 2009). Interferon alpha is considered to be a biological response modulator which strengthens natural responses of the organism to diseases. It affects both the cellular and humoral immunity. It stimulates the production of anti-cancer antibodies, activates the cytotoxic action of macrophages, NK cells and lympho-
10 cytes. INF alpha increases also the expression of HLA histocompatibility antigens on cancer cells, which facilitates their recognition by immune cells. It mediates the slowdown of growth and divisions of cancer cells, and consequently their death.

Interferon alpha has been used to treat various types of cancers, including hairy
15 cell leukemia, melanoma, kidney cancer, myeloblastic and myelocytic leukemia, lymphoma, Kaposi's sarcoma and other neoplastic diseases of the blood (Folkman J., N. Engl. J. Med.1995, 333: 1757-1763; Sidky YA, Borden EC. Cancer Res. 1987. 47: 5155-5161; Iwagak H, Hizuta A, Yoshino T, et al, Anticancer Res. 1993, 13:13-15; Rubinger M, Plenderleith IH, Lertzman M, et al, Chest. 1995,
20 108:281-282). However, at the dose required to achieve therapeutic effect in patients, toxic effects such as neutropenia, flu-like symptoms, malaise, anorexia and liver dysfunction were observed. Because of these side effects, interferon alpha therapy is often interrupted, which makes this therapy ineffective. Moreover, the biological half-life of the majority of cytokines, including
25 interferon-alpha, is short and lasts up to several hours, due to which frequent injections are needed. For various reasons, frequent use of the drug is inconvenient for the patient (especially in the long-term treatment). This resulted in the need of designing extended-release formulations of interferon-alpha.

Several attempts have been taken to improve interferon alpha properties. The
30 attempt to extend the biological half-life of interferon by providing hetero-dimeric fusions with carrier proteins comprising linkers enabling proper folding of the expressed fusion proteins is disclosed for example in US7943733. Other attempts are based on resolved structure of the biologically active form of

interferon, i.e. its naturally formed noncovalent homo-dimers which are formed by anti-parallel inter-locking of the two monomers at the receptor site a zinc ion (Zn^{2+}) (R. Radhakrishnan, Structure 1996, Vol. 4 No 12, 1453-1463). Constructs of homodimers of interferon alpha linked via glycine-serine linker are mentioned in
5 patent application LT2010012, but their activity data are not provided.

IFN γ is also known to act as noncovalently associated homodimer in which two identical polypeptide chains are oriented in an antiparallel manner to generate a symmetrical molecule (Ealick, S. E., Science (1991) 262, 698-702). Therefore, the possibility exists that IFN γ dimeric forms could occupy the receptor binding
10 site more efficient, but this hypothesis was not clinically confirmed.

Attempts to develop derivatives of alpha interferon that would be free of the above mentioned side effects resulted in the introduction to the treatment of long-acting pegylated alpha interferons. Pegylation is one of the popular methods of proteins administration into the body of mammals, aimed at reducing or
15 overcoming side effects of the active substance. The principle of pegylation is creation of a protective barrier around the modified molecules, resulting in the extended time of the desired concentration of the substance (due to the change of pharmacokinetic and pharmacodynamic properties). Absorption time is elongated and the elimination from the body is longer.

20 Values of these parameters are dependent on the structure of polyethylene glycol (PEG) molecules: chain length, linearity, degree of branching, type and number of binding sites and on number of glycol molecules attached. [Delgado C, Francis GE, Fisher D., The uses and properties of PEG-linked proteins. Crit. Rev. Ther. Drug Carrier Syst. 1992; 9 (3-4): 249-304].

25 Pegylation does not affect the manner of binding of interferon to its receptor. Preclinical studies have demonstrated that pegylated interferon alpha binds to IFN α -2a receptor and exerts the same or higher biological activity *in vitro*, as confirmed in the tests on the tumor cell culture and on mice with implanted human renal carcinoma cells [Nieforth K, Nadeau R, Patel IH, Mould D. Use of an
30 indirect pharmacodynamic stimulation model of MX protein induction to compare in vivo activity of interferon α -2a and a polyethylene glycol -modified derivative in healthy subjects, Clin. Pharmacol. Ther. 1996; 59: 636-46; Paul G, et al. Pegylated interferon - α -2b: Pharmacokinetics, pharmacodynamics, safety, and preliminary efficacy data. Clin. Pharmacol. Ther. 2000; 68: 556-67].

Despite promising data from animal model experiments, commercially available pegylated interferon-containing preparations PEGIntron® and PEGASYS® (G. Pasut, F.M. Veronese, Prog. Polym. Sci. 32 (2007) 933-961) with a 40 kDa branched and a 12 kDa linear PEG chains attached to IFN α , respectively, demonstrated safety profile qualitatively similar or even worse from the corresponding unmodified interferon molecules (Bukowski R. M. et al., *Cancer*, 95(2):389-96 (2002); Bukowski R. M. et al., *Journal of Clinical Oncology*, 20(18):3841-3949 (2002); Motzer, R. J. et al., *J. Clin. Oncol.*, 19(5): 1312-9 (2001); Tong M. J., *Journal of Interferon and Cytokine Research*, 18:81-86 (1998); Yao G. B. et al., *Journal of Gastroenterology and Hepatolog.*, 15:1165-1170 (2000); Heathcote E. J. et al, *N. Engl. J. Med.*, 343(23):1673-80 (2000); Tong M. J. et al., *Hepatology*; 26(3):747-54 (1997)).

The most frequently observed side effects of pegylated IFN α therapy include: dose-dependent nausea, anorexia, stiffening of the muscles. In addition, longer therapy revealed dose-limiting, such as severe fatigue, neurotoxicity, liver malfunctioning and inhibition of bone marrow functions (PEG-Intron® at doses of 7.5 μ g/kg and higher) (Bukowski R. M. et al., *Cancer*; 95(2):389-96 (2002)).

Therefore, despite the existence of clinically employed anti-cancer therapies based on both the TRAIL protein and proteins of the interferons family (also modified, in particular by pegylation), they are not sufficiently effective and have many well-known disadvantages, of which one of the most severe and restricting is limited effectiveness of treatment, lack of selectivity against cancer cells, side effects and primary or acquired resistance. There is still a need for improved cancer therapy based both on the activity of interferon and TRAIL protein, that would be both effective and selective *in vivo* against cancer cells. There remains an urgent and unmet need for new anticancer agents that would allow both to broaden the range of available agents and to find agents that are more effective (cytotoxic) and selective. There is also a need for new selective agents with increased stability and improved pharmacokinetics.

Certain exemplary embodiments provide a fusion protein comprising: domain (a) which is a functional fragment of hTRAIL protein sequence (SEQ. No. 16), which fragment begins with an amino acid at a position not lower than hTRAIL95, or a homolog of said functional fragment having at least 70% sequence identity; and domain (b) which is a sequence of an immunostimulating effector peptide,

selected from the group consisting of the pseudodimer of interferon gamma of SEQ. No. 19, and the pseudodimer of interferon alpha 2b of SEQ. No. 46; wherein the sequence of domain (b) is attached at the C-terminus or N-terminus of domain (a).

- 5 Other exemplary embodiments provide a fusion protein comprising: domain (a) which is a functional fragment of hTRAIL protein sequence, which fragment begins with an amino acid at a position from the range hTRAIL95 to hTRAIL122, inclusive, and ends with the amino acid hTRAIL281, or a homolog of said functional fragment having at least 70% sequence identity, wherein said
- 10 functional fragment or homolog thereof binds to receptors on the surface of mammalian cells and induces an apoptotic signal in the cells, and wherein hTRAIL protein has the amino acid sequence set forth as SEQ. No. 16; and domain (b) which is a sequence of an immunostimulating effector peptide, selected from the group consisting of the pseudodimer of interferon gamma with
- 15 an amino acid sequence consisting of SEQ. No. 19, and the pseudodimer of interferon alpha 2b with an amino acid sequence consisting of SEQ. No. 46; wherein the sequence of domain (b) is attached at the C-terminus or N-terminus of domain (a).

Also provided are polynucleotides encoding the fusion protein and expression

20 vectors and host cells for expression of the fusion protein from the polynucleotide.

Further provided are uses of the fusion protein and pharmaceutical compositions comprising the fusion peptide, for treatment of cancer.

Selected embodiments provide a solution of this problem by means of novel

25 fusion proteins that incorporate a domain derived from TRAIL and a short effector peptide domain having the immune system stimulating activity, which effector peptide does not include TRAIL fragments, wherein the effector peptide potentiates or complements the action of TRAIL. Moreover, it turned out that in many cases the fusion proteins of selected embodiments are more potent than

30 soluble TRAIL and its variants consisting of fragments of its sequence, as well as more potent than respective effector peptides. In many cases, novel fusion

proteins also overcome resistance to TRAIL. Moreover, the incorporation of the effector peptide results in prolonged half-life and increased retention of protein in the tumor and its enhanced efficiency. Additionally, in certain variants novel fusion proteins may be able to link PEG, which has protective effect against non-specific proteases and additionally alters pharmacokinetic and pharmacodynamic properties, particularly with respect to prolongation of the biological half-life.

Description of Figures

Selected embodiments will now be described in detail with reference to the Figures of the drawing.

Fig. 1 presents schematic structures of fusion proteins of the invention according to Ex. 1, Ex.2, Ex. 3 and Ex. 4.

Fig. 2 presents schematic structures of fusion proteins of the invention according to Ex. 5, Ex. 6, Ex. 7, Ex. 8, Ex. 9, Ex. 10 and Ex. 11.

Fig. 3 presents schematic structures of fusion proteins of the invention according to Ex. 12, Ex. 13, Ex. 14 and Ex. 15.

Fig. 4 presents schematic structures of fusion proteins of the invention according to Ex. 16 and Ex. 17.

Fig. 5 shows circular dichroism spectra for rhTRAIL114-281, rhTRAIL95-281 and fusion proteins of Ex. 12, Ex. 5, Ex. 3 and Ex. 14 expressed in specific ellipticity.

Fig. 6 presents tumor volume changes (% of initial stage) in Crl:CD1-Foxn1nu mice burdened with colon cancer HCT116, treated with fusion proteins of the invention of Ex. 3, Ex. 12 and Ex. 14 compared to rhTRAIL114-281.

Fig. 7 presents the tumor growth inhibition values (%TGI) in Crl:CD1-Foxn1^{nu} 1 mice burdened with colon cancer HCT116, treated with fusion proteins of the invention of Ex.3, Ex. 12 and Ex. 14 compared to rhTRAIL114-281.

Fig. 8 presents tumor volume changes (% of initial stage) in Crl:SHO-PrkdcscidHrhr mice burdened with colon cancer HCT116 treated with fusion protein of the invention of Ex. 14 compared to rhTRAIL114-281.

Fig. 9 presents the tumor growth inhibition values (%TGI) in Crl:SHO-PrkdcscidHrhr mice burdened with colon cancer HCT116 treated with fusion protein of the invention of Ex. 14 compared to rhTRAIL114-281.

Fig. 10 presents tumor volume changes(% of initial stage) in Crl:SHO-PrkdcscidHrhr mice burdened with liver cancer PLC/PRF/5 treated with fusion protein of the invention of Ex. 14 compared to rhTRAIL114-281.

Fig. 11 presents the tumor growth inhibition values (%TGI) in Crl:SHO-PrkdcscidHrhr mice burdened with liver cancer PLC/PRF/5 treated with fusion protein of the invention of Ex. 14 compared to rhTRAIL114-281.

Fig. 12 presents tumor volume changes(% of initial stage) in Crl:SHO-PrkdcscidHrhr mice burdened with liver cancer HepG2, treated with fusion protein of the invention of Ex. 14 compared to rhTRAIL114-281.

Fig. 13 presents the tumor growth inhibition values (%TGI) in Crl:SHO-PrkdcscidHrhr mice burdened with liver cancer HepG2 treated with fusion protein of the invention of Ex. 14 compared to rhTRAIL114-281.

Detailed Description of the Invention

The invention relates to a fusion protein comprising:

domain (a) which is the functional fragment of a sequence of soluble hTRAIL protein, which fragment begins with an amino acid at a position not lower than hTRAIL95, or a homolog of said functional fragment having at least 70% sequence identity, and

domain (b) which is a sequence of an immunostimulating effector peptide, wherein the sequence of the domain (b) is attached at the C-terminus and/or N-terminus of domain (a).

The term “the functional soluble fragment of a sequence of soluble hTRAIL” should be understood as denoting any such fragment of soluble hTRAIL that is capable of inducing apoptotic signal in mammalian cells upon binding to its receptors on the surface of the cells.

It will be also appreciated by a skilled person that the existence of at least 70% homology of the TRAIL sequence is known in the art.

It should be understood that domain (b) of the effector peptide in the fusion protein of the invention is neither hTRAIL protein nor a part or fragment of hTRAIL protein.

5 The term "peptide" in accordance with the invention should be understood as a molecule built from plurality of amino acids linked together by means of a peptide bond. Thus, the term "peptide" according to the invention includes oligopeptides, polypeptides and proteins.

10 In the present invention the amino acid sequences of peptides will be presented in a conventional manner adopted in the art, i.e. in the direction from N-terminus (N-end) of the peptide towards its C-terminus (C-end). Any sequence will thus have its N-terminus on the left side and C-terminus on the right side of its linear presentation.

The fusion protein of the invention may incorporate a single domain (b) of the effector peptide, attached at the C-terminus or N-terminus of domain (a).

15 In a particular embodiment, the domain (a) is a fragment of hTRAIL sequence, beginning with an amino acid from the range of hTRAIL95 to hTRAIL122, inclusive, and ending with the amino acid hTRAIL 281.

In particular, domain (a) may be selected from the group consisting of sequences corresponding to hTRAIL95-281, hTRAIL114-281, hTRAIL116-281, hTRAIL120-281, 20 hTRAIL121-281 and hTRAIL122-281. It will be evident to those skilled in the art that hTRAIL95-281, hTRAIL114-281, hTRAIL116-281, hTRAIL120-281, hTRAIL121-281 and hTRAIL122-281 represent a fragment of human TRAIL protein starting with amino acid marked with the number 95, 114, 116, 120, 121 and 122, respectively, in the known sequence of hTRAIL published in GenBank under 25 Accession No P50591.

In another particular embodiment, the domain (a) is a homolog of the functional fragment of soluble hTRAIL protein sequence beginning at amino acid position not lower than hTRAIL95 and ending at amino acid hTRAIL281, the sequence of which is at least in 70%, preferably in 85%, identical to original sequence.

30 In specific variants of this embodiment the domain (a) is a homolog of a fragment selected from the group consisting of sequences corresponding to

hTRAIL95-281, hTRAIL114-281, hTRAIL116-281, hTRAIL120-281, hTRAIL121-281 and hTRAIL122-281.

It should be understood that a homolog of a hTRAIL fragment is a variation/modification of the amino acid sequence of this fragment, wherein at least one amino acid is changed, including 1 amino acid, 2 amino acids, 3 amino acids, 4 amino acids, 5 amino acids, 6 amino acids, and not more than 15% of amino acids, and wherein a fragment of the modified sequence has preserved functionality of the hTRAIL sequence, i.e. the ability of binding to cell surface death receptors and inducing apoptosis in mammalian cells. Modification of the amino acid sequence may include, for example, substitution, deletion, truncation and/or addition of amino acids.

Preferably, the homolog of hTRAIL fragment having modified sequence shows modified affinity to the death receptors DR4 (TRAIL-R1) or DR5 (TRAIL-R2) in comparison with the native fragment of hTRAIL.

The term "modified affinity" refers to increased affinity and/or affinity with altered receptor selectivity.

Preferably, the homolog of the fragment of hTRAIL having modified sequence shows increased affinity to the death receptors DR4 and DR5 compared to native fragment of hTRAIL.

Particularly preferably, the homolog of fragment of hTRAIL having modified sequence shows increased affinity to the death receptor DR5 in comparison with the death receptor DR4, i.e. an increased selectivity DR5/DR4.

Also preferably, the homolog of fragment of hTRAIL having modified sequence shows an increased selectivity towards the death receptors DR4 and/or DR5 in relation to the affinity towards the receptors DR1 (TRAIL-R3) and/or DR2 (TRAIL-R4).

Modifications of hTRAIL resulting in increased affinity and/or selectivity towards the death receptors DR4 and DR5 are known to those skilled in the art, for example from the publication Tur V, van der Sloot AM, Reis CR, Szegezdi E, Cool RH, Samali A, Serrano L, Quax WJ. DR4-selective tumor necrosis factor-related apoptosis-inducing ligand (TRAIL) variants obtained by structure-based design. J. Biol. Chem. 2008 Jul 18;283(29):20560-8, which describes the D218H mutation

having increased selectivity towards DR4, or Gasparian ME, Chernyak BV, Dolgikh DA, Yagolovich AV, Popova EN, Sycheva AM, Moshkovskii SA, Kirpichnikov MP. Generation of new TRAIL mutants DR5-A and DR5-B with improved selectivity to death receptor 5, Apoptosis. 2009 Jun;14(6):778-87, which describes the D269H mutation having a reduced affinity towards DR4. hTRAIL mutants resulting in increased affinity towards one receptor selected from the DR4 and DR5 comparing with DR1 and DR2 receptors and increased affinity towards the receptor DR5 comparing with DR4 are also described in WO2009077857 and WO2009066174.

- 10 Suitable mutations are one or more mutations in the positions of native hTRAIL selected from the group consisting of 131, 149, 159, 193, 199, 201, 204, 204, 212, 215, 218 and 251, in particular, mutations involving the substitution of an amino acid with a basic amino acid such as lysine, histidine or arginine, or amino acid such as glutamic acid or aspartic acid. Particularly one or more mutations selected from the group consisting of G131R, G131K, R149I, R149M, R149N, R149K, S159R, Q193H, Q193K, N199H, N199R, K201H, K201R, K204E, K204D, K204L, K204Y, K212R, S215E, S215H, S215K, S215D, D218Y, D218H, K251D, K251E and K251Q, as described in WO2009066174, may be specified.

- 20 Suitable mutations are also one or more mutations in the positions of native hTRAIL selected from the group consisting of 195, 269 and 214, particularly mutations involving the substitution of an amino acid with a basic amino acid such as lysine, histidine or arginine. Particularly one or more mutations selected from the group consisting of D269H, E195R, and T214R, as described in WO2009077857, may be specified.

- 25 In a particular embodiment, the domain (a) which is a homolog of the fragment of hTRAIL is selected from D218H mutant of the native TRAIL sequence, as described in WO2009066174, or the Y189N-R191K-Q193R-H264R-I266R-D269H mutant of the native TRAIL sequence, as described in Gasparian ME, Chernyak BV, Dolgikh DA, Yagolovich AV, Popova EN, Sycheva AM, Moshkovskii SA, Kirpichnikov MP., Apoptosis. 2009 Jun;14(6):778-87.

The immunostimulating effector peptide of domain (b) may be a cytokine peptide which among others intensely stimulates human monocytes to produce TRAIL protein, thus significantly affecting the ability to eliminate cancer cells.

In one embodiment of the fusion protein of the invention, the effector peptide is a peptide having immunostimulating activity selected from the group consisting of SEQ. No. 17 (derived from INF alpha 2b), SEQ. No. 18 (derived from INF gamma), SEQ. No. 19 (a pseudodimer of INF gamma), SEQ. No. 46 (a
 5 pseudodimer of interferon alpha 2b) and SEQ. No. 47 (the consensus sequence of interferon alpha).

The effector peptide of the above group is the peptide that stimulates TRAIL overexpression, and specifically the 165-amino acid fragment of interferon alpha - subunit beta presented by SEQ. No. 17.

10 It is believed that the peptide comprising sequence of interferon alpha beta subunit incorporated into the fusion protein of the invention will effectively eliminate cancer cells.

Another effector peptide is a 124-amino acid fragment of interferon gamma presented by SEQ. No. 18.

15 It is believed that the peptide comprising sequence of interferon gamma incorporated into the fusion protein of the invention will effectively eliminate cancer cells.

The effector peptide of the above group is a 263-amino acid peptide constituting
 20 a fusion of two human interferon gamma subunits, forming single-chain pseudodimer of INF gamma, described by Landar'a et al. (J.Mol.Biol. 299: 169-179, 2000). The resulting single-chain protein variant retains the ability to bind to the suitable receptor and biological activity expected for interferon-gamma. This effector peptide is presented by SEQ. No. 19.

Another effector peptide of the above group is a 351-amino acid peptide, a fusion
 25 of two human interferon alpha 2b subunits forming single-chain pseudodimer of INF alpha 2b wherein the second chain of IFN alpha 2b subunit sequence is reversed comparing to the native sequence (i.e. from C-terminus to N-terminus). The resulting effector peptide is characterized by two "native" C-terminal ends of interferon alpha 2b bound to each other. Monomers in naturally forming IFN
 30 alpha dimers are linked by their C-terminal ends. N-terminal ends, in turn, are responsible for interaction with the receptor and provide a proper environment for co-ordination of the process of dimerization of the zinc ion (glutamic acid residues 41 and 42). The resulting single-chain protein variant retains the ability

to bind to the suitable receptor and biological activity expected for interferon-alpha. This effector peptide is presented by the SEQ. No. 46.

Another effector peptide is a 166-amino acid consensus sequence of interferon alpha presented by SEQ. No. 47. This consensus sequence is disclosed in US
5 4,695,623.

It is believed that the peptide comprising the consensus sequence of interferon alpha incorporated into the fusion protein of the invention will effectively eliminate cancer cells.

Upon binding to TRAIL receptors present on the surface of cancer cells, the
10 fusion protein will exert a double effect. Domain (a), that is a functional fragment of TRAIL or its homolog with preserved functionality, will exert its known agonistic activity - i.e. binding to death receptors on the cell surface and activation of the extrinsic pathway of apoptosis. After internalization of the fusion protein comprising immunostimulating peptide, the domain (b) will be
15 able to potentially exert its action intracellularly in parallel to the activity of TRAIL domain. In this way, anti-cancer activity of TRAIL can be potentiated by activation of other elements and mechanisms -such as stimulation of B cells to produce antibodies, stimulation of caspase 7 and 8 expression, or stimulation of overexpression of TRAIL.

20 In one of the embodiments of the invention, domain (a) and domain (b) are linked by at least one domain (c) comprising the sequence of a protease cleavage site recognized by proteases present in the cell environment, especially in the tumor cell environment. The linkage of the domain (a) with the domain (b) by at least one domain (c) means that between domains (a) and (b) more
25 than one domain (c) may be present, in particular one or two domains (c).

A protease cleavage site can be selected from:

- a sequence recognized by metalloprotease MMP, in particular Pro Leu Gly Leu Ala Gly (PLGLAG in one-letter convention) designated as SEQ. No. 20,
 - 30 - a sequence recognized by urokinase uPA, in particular Arg Val Val Arg (RVVR in one-letter convention) designated as SEQ.No. 21,
- and their combinations.

In one of the embodiments of the invention, the protease cleavage site is a combination of the sequence recognized by metalloprotease MMP and the sequence recognized by urokinase uPA, located next to each other in any order.

In one embodiment, the domain (c) is a combination of MMP/uPA (SEQ. No 20/Sekw. No. 21), that is the sequence Pro Leu Gly Leu Ala Gly Arg Val Val Arg (PLGLAGRVVR in one letter convention), or a combination of uPA/MMP (SEQ. No 21/SEQ. No. 20), that is the sequence Arg Val Val Arg Pro Leu Gly Leu Ala Gly (RVVRPLGLAG in one letter convention). Such combinations may be repeated, preferably twice.

10 Proteases metalloprotease MMP and urokinase uPA are overexpressed in the tumor environment. The presence of the sequence recognized by the proteases enables cleavage of the domain (a) from the domain (b) upon internalization of the construct, i.e. the release of the functional domain (b) and thus its activation.

15 The presence of the protease cleavage site, by allowing quick release of the effector peptide, increases the chances of transporting the peptide to the place of its action before random degradation of the fusion protein by proteases present in the cell occurs.

In another embodiment, between the domains (a) and (b) there is additionally incorporated domain (d) of a sequence suitable for attachment of a PEG molecule (PEG linker) to the fusion protein of the invention.

Such a PEG linker is for example a known sequence Ala Ser Gly Cys Gly Pro Glu (ASGCGPE in a one-letter convention), designated as the SEQ. No. 22. PEG linker can be also chosen from among Ala Ala Cys Ala Ala (AACAA in a one-letter convention), Ser Gly Gly Cys Gly Gly Ser (SGGCGGS in a one-letter convention) and Ser Gly Cys Gly Ser (SGCGS in a one-letter convention), designated as, respectively, SEQ. No. 23, SEQ. No. 24 and SEQ. No. 25.

In one of the embodiments, the protein of the invention comprises both domain (c) and domain (d).

30 In a preferred embodiment, domain (d) is located between two domains (c), in particular between two domains (c), which are selected from the protease cleavage site and a combination of protease cleavage sites, in particular, the

sequence recognized by metalloproteases MMP (SEQ. No. 20), the sequence recognized by urokinase uPA (SEQ. No. 21), and the combination MMP/uPA (SEQ. No. 20/ SEQ. No. 21) or uPA/MMP (SEQ. No. 21/ SEQ. No. 20).

Thus, in one embodiment of the fusion protein of the invention, the protease
5 cleavage site is a combination of the sequence recognized by metalloprotease MMP and the sequence recognized by urokinase uPA, in any order, separated by the PEG linker sequence discussed above.

It should be understood that in the case when the fusion protein has both the domain (d) of the PEG linker and the domains (c) of the cleavage site between
10 the domains (a) and (b), then the domains (c) are located in such a way that after cleavage of the construct the domain (d) is disconnected from the domains (a) and (b). These two domains (c) may contain both single protease cleavage site and combinations thereof, as defined above. In other words, if the fusion protein contains both domain (d) comprising PEG linker and cleavage site
15 domains (c), then domain (d) is located between domains (c). The invention does not comprise such a variant in which domain (d) would be located between domain (c) and domain (a) or between domain (c) and domain (b), that is the variant wherein after cleavage of the construct the sequence suitable for attachment to the fusion protein of the invention of a PEG molecule (d) would
20 remain attached to domain (a) or domain (b).

PEG molecules useful for attachment to the fusion protein may be selected from linear and branched PEG molecules. Particularly useful are linear PEG molecule having a molecular weight between 4000 and 20000.

Apart from the main functional elements of the fusion protein, the cleavage site
25 domain(s) and the PEG linker sequence, the fusion proteins of the invention may contain a neutral sequence/sequences of a flexible steric glycine-serine linker (spacer). Such linkers/spacers are well known and described in the literature. Their incorporation into the sequence of the fusion protein is intended to provide the correct folding of proteins produced by the process of its
30 overexpression in the host cells.

Flexible steric linker may be selected from any combination of glycine and serine residues. In particular, flexible linker may be selected from the group consisting of Gly Ser Gly Gly Gly (GSGGG in one letter convention),

Gly Gly Gly Ser (GGGS in one letter convention), Xaa Gly Gly Ser (XGGS in one letter convention) wherein Xaa designates any amino acid or is absent, and Gly Gly Ser Gly (GGSG in one letter convention) designated as, respectively SEQ. No. 26, SEQ. No. 27 and SEQ. No. 28) and SEQ. No. 50.

- 5 Particular embodiments of the fusion protein of the invention are fusion proteins comprising an immunostimulating peptide selected from the group consisting of the proteins represented by SEQ. No. 1, SEQ. No. 2, SEQ. No. 3, SEQ. No. 4, and SEQ. No. 45.

- 10 Other specific embodiment of the fusion protein of the invention is fusion protein comprising an immunostimulating peptide represented by SEQ. No. 44.

Other specific embodiments of the fusion protein of the invention are fusion proteins comprising an immunostimulating peptide, selected from the group consisting of the proteins represented by SEQ. No. 5, SEQ. No. 6, SEQ. No. 7, SEQ. No. 8, SEQ. No. 9, SEQ. No. 10 and SEQ. No. 11.

- 15 Other specific embodiments of the fusion protein of the invention are fusion proteins comprising an immunostimulating peptide, selected from the group consisting of the proteins represented by SEQ. No. 12, SEQ. No. 13, SEQ. No. 14 and SEQ. No. 15.

- 20 A detailed description of the structure of representative fusion proteins mentioned above are shown in Figures 1 to 3 and in Fig. 4, and in the Examples presented herein below.

- 25 In accordance with the present invention, "a fusion protein" means a single protein molecule containing two or more proteins or fragments thereof, covalently linked via peptide bond within their respective peptide chains, without additional chemical linkers.

The fusion protein can also be alternatively described as a protein construct or a chimeric protein. According to the present invention, the terms "construct" or "chimeric protein", if used, should be understood as referring to the fusion protein as defined above.

- 30 For a person skilled in the art it will be apparent that the fusion protein thus defined can be synthesized by known methods of chemical synthesis of peptides and proteins.

The fusion protein can be synthesized by methods of chemical peptide synthesis, especially using the techniques of peptide synthesis in solid phase using suitable resins as carriers. Such techniques are conventional and known in the art, and described inter alia in the monographs, such as for example Bodanszky and
5 Bodanszky, The Practice of Peptide Synthesis, 1984, Springer- Verlag, New York, Stewart et al., Solid Phase Peptide Synthesis, 2nd Edition, 1984, Pierce Chemical Company.

The fusion protein can be synthesized by the methods of chemical synthesis of peptides as a continuous protein. Alternatively, the individual fragments
10 (domains) of protein may be synthesized separately and then combined together in one continuous peptide via a peptide bond, by condensation of the amino terminus of one peptide fragment from the carboxyl terminus of the second peptide. Such techniques are conventional and well known.

For verification of the structure of the resulting peptide known methods of the
15 analysis of amino acid composition of peptides may be used, such as high resolution mass spectrometry technique to determine the molecular weight of the peptide. To confirm the peptide sequence protein sequencers can also be used, which sequentially degrade the peptide and identify the sequence of amino acids.

20 Preferably, however, the fusion protein of the invention is a recombinant protein, generated by methods of gene expression of a polynucleotide sequence encoding the fusion protein in host cells.

A further aspect of the invention is the polynucleotide sequence, particularly DNA sequence encoding a fusion protein as defined above.

25 Preferably, the polynucleotide sequence, particularly DNA, according to the invention, encoding the fusion protein as defined above, is a sequence optimized for expression in *E. coli*.

Another aspect of the invention is also an expression vector containing the polynucleotide sequence, particularly DNA sequence of the invention as defined
30 above.

Another aspect of the invention is also a host cell comprising an expression vector as defined above.

A preferred host cell for expression of fusion proteins of the invention is an *E. coli* cell.

Methods for generation of recombinant proteins, including fusion proteins, are well known. In brief, this technique consists in generation of polynucleotide molecule, for example DNA molecule encoding the amino acid sequence of the target protein and directing the expression of the target protein in the host. Then, the target protein encoding polynucleotide molecule is incorporated into an appropriate expression vector, which ensures an efficient expression of the polypeptide. Recombinant expression vector is then introduced into host cells for transfection/transformation, and as a result a transformed host cell is produced. This is followed by a culture of transformed cells to overexpress the target protein, purification of obtained proteins, and optionally cutting off by cleavage the tag sequences used for expression or purification of the protein.

Suitable techniques of expression and purification are described, for example in the monograph Goeddel, Gene Expression Technology, Methods in Enzymology 185, Academic Press, San Diego, CA (1990), and A. Staron et al., Advances Mikrobiol., 2008, 47, 2, 1983-1995.

Cosmids, plasmids or modified viruses can be used as expression vectors for the introduction and replication of DNA sequences in host cells. Typically plasmids are used as expression vectors. Suitable plasmids are well known and commercially available.

Expression vector of the invention comprises a polynucleotide molecule encoding the fusion protein of the invention and the necessary regulatory sequences for transcription and translation of the coding sequence incorporated into a suitable host cell. Selection of regulatory sequences is dependent on the type of host cells and can be easily carried out by a person skilled in the art. Examples of such regulatory sequences are transcriptional promoter and enhancer or RNA polymerase binding sequence, ribosome binding sequence, containing the transcription initiation signal, inserted before the coding sequence, and transcription terminator sequence, inserted after the coding sequence. Moreover, depending on the host cell and the vector used, other sequences may be introduced into the expression vector, such as the origin of replication,

additional DNA restriction sites, enhancers, and sequences allowing induction of transcription.

- The expression vector will also comprise a marker gene sequence, which confers defined phenotype to the transformed cell and enables specific selection of transformed cells. Furthermore, the vector may also contain a second marker sequence which allows to distinguish cells transformed with recombinant plasmid containing inserted coding sequence of the target protein from those which have taken up the plasmid without insert. Most often, typical antibiotic resistance markers are used, however, any other reporter genes known in the field may be used, whose presence in a cell (in vivo) can be easily determined using autoradiography techniques, spectrophotometry or bio- and chemiluminescence. For example, depending on the host cell, reporter genes such as β -galactosidase, β -glucuronidase, luciferase, chloramphenicol acetyltransferase or green fluorescent protein may be used.
- Furthermore, the expression vector may contain signal sequence, transporting proteins to the appropriate cellular compartment, e.g. periplasm, where folding is facilitated. Additionally a sequence encoding a label/tag, such as HisTag attached to the N-terminus or GST attached to the C-terminus, may be present, which facilitates subsequent purification of the protein produced using the principle of affinity, via affinity chromatography on a nickel column. Additional sequences that protect the protein against proteolytic degradation in the host cells, as well as sequences that increase its solubility may also be present.

- Auxiliary element attached to the sequence of the target protein may block its activity, or be detrimental for another reason, such as for example due to toxicity. Such element must be removed, which may be accomplished by enzymatic or chemical cleavage. In particular, a six-histidine tag HisTag or other markers of this type attached to allow protein purification by affinity chromatography should be removed, because of its described effect on the liver toxicity of soluble TRAIL protein. Heterologous expression systems based on various well-known host cells may be used, including prokaryotic cells: bacterial, such as *Escherichia coli* or *Bacillus subtilis*, yeasts such as *Saccharomyces*

cerevisiae or *Pichia pastoris*, and eukaryotic cell lines (insect, mammalian, plant).

Preferably, due to the ease of culturing and genetic manipulation, and a large amount of obtained product, the *E. coli* expression system is used. Accordingly, the polynucleotide sequence containing the target sequence encoding the fusion protein of the invention will be optimized for expression in *E. coli*, i.e. it will contain in the coding sequence codons optimal for expression in *E. coli*, selected from the possible sequence variants known in the state of art. Furthermore, the expression vector will contain the above described elements suitable for *E. coli* attached to the coding sequence.

Accordingly, in a preferred embodiment of the invention a polynucleotide sequence comprising a sequence encoding a fusion protein of the invention, optimized for expression in *E. coli* is selected from the group of polynucleotide sequences consisting of:

SEQ. No. 29 SEQ. No. 30; SEQ. No. 31; SEQ. No. 32; SEQ. No. 33; SEQ. No. 34; SEQ. No. 35; SEQ. No. 36; SEQ. No. 37; SEQ. No. 38; SEQ. No. 39; SEQ. No. 40; SEQ. No. 41, SEQ. No. 42, SEQ. No. 43, SEQ. No. 48 and SEQ. No. 49,

which encode a fusion protein having an amino acid sequence corresponding to amino acid sequences selected from the group consisting of amino acid sequences, respectively:

SEQ. No. 1; SEQ. No. 2; SEQ. No. 3; SEQ. No. 4; SEQ. No. 5; SEQ. No. 6; SEQ. No. 7; SEQ. No. 8; SEQ. No. 9; SEQ. No. 10; SEQ. No. 11; SEQ. No. 12; SEQ. No. 13; SEQ. No. 14 and SEQ. No. 15., SEQ. No. 44 and SEQ. No. 45. In a preferred embodiment, the invention provides also an expression vector suitable for transformation of *E. coli*, comprising the polynucleotide sequence selected from the group of polynucleotide sequences SEQ. No. 29 to SEQ. No. 43, SEQ. No. 48 and SEQ. No. 49 indicated above, as well as *E. coli* cell transformed with such an expression vector.

Transformation, i.e. introduction of a DNA sequence into bacterial host cells, particularly *E. coli*, is usually performed on the competent cells, prepared to take up the DNA for example by treatment with calcium ions at low temperature (4°C), and then subjecting to the heat-shock (at 37-42°C) or by electroporation.

Such techniques are well known and are usually determined by the manufacturer of the expression system or are described in the literature and manuals for laboratory work, such as Maniatis et al., *Molecular Cloning*. Cold Spring Harbor, N.Y., 1982).

- 5 The procedure of overexpression of fusion proteins of the invention in *E. coli* expression system will be further described below.

The invention also provides a pharmaceutical composition containing the fusion protein of the invention as defined above as an active ingredient and a suitable pharmaceutically acceptable carrier, diluent and conventional auxiliary components. The pharmaceutical composition will contain an effective amount of the fusion protein of the invention and pharmaceutically acceptable auxiliary components dissolved or dispersed in a carrier or diluent, and preferably will be in the form of a pharmaceutical composition formulated in a unit dosage form or formulation containing a plurality of doses. Pharmaceutical forms and methods of their formulation as well as other components, carriers and diluents are known to the skilled person and described in the literature. For example, they are described in the monograph Remington's Pharmaceutical Sciences, ed. 20, 2000, Mack Publishing Company, Easton, USA.

The terms "pharmaceutically acceptable carrier, diluent, and auxiliary ingredient" comprise any solvents, dispersion media, surfactants, antioxidants, stabilizers, preservatives (e.g. antibacterial agents, antifungal agents), isotonicity agents, known in the art. The pharmaceutical composition of the invention may contain various types of carriers, diluents and excipients, depending on the chosen route of administration and desired dosage form, such as liquid, solid and aerosol forms for oral, parenteral, inhaled, topical, and whether that selected form must be sterile for administration route such as by injection. The preferred route of administration of the pharmaceutical composition according to the invention is parenteral, including injection routes such as intravenous, intramuscular, subcutaneous, intraperitoneal, intratumor, or by single or continuous intravenous infusions.

In one embodiment, the pharmaceutical composition of the invention may be administered by injection directly to the tumor. In another embodiment, the pharmaceutical composition of the invention may be administered intravenously.

In yet another embodiment, the pharmaceutical composition of the invention can be administered subcutaneously or intraperitoneally. A pharmaceutical composition for parenteral administration may be a solution or dispersion in a pharmaceutically acceptable aqueous or non-aqueous medium, buffered to an appropriate pH and isoosmotic with body fluids, if necessary, and may also contain antioxidants, buffers, bacteriostatic agents and soluble substances, which make the composition compatible with the tissues or blood of recipient. Other components, which may be included in the composition, are for example water, alcohols such as ethanol, polyols such as glycerol, propylene glycol, liquid polyethylene glycol, lipids such as triglycerides, vegetable oils, liposomes. Proper fluidity and the particles size of the substance may be provided by coating substances, such as lecithin, and surfactants, such as hydroxypropyl-cellulose polysorbates, and the like.

Suitable isotonicity agents for liquid parenteral compositions are, for example, sugars such as glucose, and sodium chloride, and combinations thereof.

Alternatively, the pharmaceutical composition for administration by injection or infusion may be in a powder form, such as a lyophilized powder for reconstitution immediately prior to use in a suitable carrier such as, for example, sterile pyrogen-free water.

The pharmaceutical composition of the invention for parenteral administration may also have the form of nasal administration, including solutions, sprays or aerosols. Preferably, the form for intranasal administration will be an aqueous solution and will be isotonic or buffered to maintain the pH from about 5.5 to about 6.5, so as to maintain a character similar to nasal secretions. Moreover, it will contain preservatives or stabilizers, such as in the well-known intranasal preparations.

The composition may contain various antioxidants which delay oxidation of one or more components. Furthermore, in order to prevent the action of micro-organisms, the composition may contain various antibacterial and antifungal agents, including, for example, and not limited to, parabens, chlorobutanol, thimerosal, sorbic acid, and similar known substances of this type. In general, the pharmaceutical composition of the invention can include, for example at least about 0.01 wt% of active ingredient. More particularly, the composition

may contain the active ingredient in the amount from 1% to 75% by weight of the composition unit, or for example from 25% to 60% by weight, but not limited to the indicated values. The actual amount of the dose of the composition according to the present invention administered to patients, including man, will
5 be determined by physical and physiological factors, such as body weight, severity of the condition, type of disease being treated, previous or concomitant therapeutic interventions, the patient and the route of administration. A suitable unit dose, the total dose and the concentration of active ingredient in the composition is to be determined by the treating physician.

10 The composition may for example be administered at a dose of about 1 microgram/kg of body weight to about 1000 mg/kg of body weight of the patient, for example in the range of 5 mg/kg of body weight to 100 mg/kg of body weight or in the range of 5 mg/kg of body weight to 500 mg/kg of body weight. The fusion protein and the compositions containing it exhibit anticancer
15 or antitumor and can be used for the treatment of cancer diseases. The invention also provides the use of the fusion protein of the invention as defined above for treating cancer diseases in mammals, including humans. The invention also provides a method of treating cancer diseases in mammals, including humans, comprising administering to a subject in need of such treatment an
20 anticancer effective amount of the fusion protein of the invention as defined above, optionally in the form of appropriate pharmaceutical composition.

The fusion protein of the invention can be used for the treatment of hematologic malignancies, such as leukemia, granulomatosis, myeloma and other hematologic malignancies. The fusion protein can also be used for the treatment of solid
25 tumors, such as breast cancer, lung cancer, including non-small cell lung cancer, colon cancer, pancreatic cancer, ovarian cancer, bladder cancer, prostate cancer, kidney cancer, brain cancer, and the like. Appropriate route of administration of the fusion protein in the treatment of cancer will be in particular parenteral route, which consists in administering the fusion protein of the invention in
30 the form of injections or infusions, in the composition and form appropriate for this administration route. The invention will be described in more detail in the following general procedures and examples of specific fusion proteins.

General procedure for overexpression of the fusion protein

Preparation of plasmid

Amino acid sequence of the target fusion protein was used as a template to generate a DNA sequence encoding it, comprising codons optimized for expression in *Escherichia coli*. Such a procedure allows to increase the efficiency of a further step of target protein synthesis in *Escherichia coli*. Resulting nucleotide sequence was then automatically synthesized. Additionally, the cleavage sites of restriction enzymes NdeI (at the 5'-end of leading strand) and XhoI (at the 3'-end of leading strand) were added to the resulting gene encoding the target protein.

These were used to clone the gene into the vector pET28a (Novagen). They may be also be used for cloning the gene encoding the protein to other vectors. Target protein expressed from this construct was equipped at the N-terminus with a polyhistidine tag (six histidines), preceded by a site recognized by thrombin, which subsequently served to its purification via affinity chromatography.

The correctness of the resulting construct was confirmed firstly by restriction analysis of isolated plasmids using the enzymes NdeI and XhoI, followed by automatic sequencing of the entire reading frame of the target protein. The primers used for sequencing were complementary to the sequences of T7 promoter (5'- TAATACGACTCACTATAGG-3') and T7 terminator (5'- GCTAGTTATTGCTCAGCGG-3 ') present in the vector. Resulting plasmid was used for overexpression of the target fusion protein in a commercial *E. coli* strain, which was transformed according to the manufacturer's recommendations. Colonies obtained on the selection medium (LB agar, kanamycin 50 µg/ml, 1% glucose) were used for preparing an overnight culture in LB liquid medium supplemented with kanamycin (50 µg/ml) and 1% glucose. After about 15h of growth in shaking incubator, the cultures were used to inoculate the appropriate culture.

Overexpression and purification of fusion proteins - general procedure A

LB medium with kanamycin (30 µg/ml) and 100 µM zinc sulfate was inoculated with overnight culture. The culture was incubated at 37°C until the optical density (OD) at 600 nm reached 0.60-0.80. Then IPTG was added to the final concentration in the range of 0.25 -1mM. After incubation (3.5 - 20h) with shaking at 25°C the culture was centrifuged for 25 min at 6,000 g. Bacterial pel-

lets were resuspended in a buffer containing 50 mM KH_2PO_4 , 0.5 M NaCl, 10 mM imidazole, pH 7.4. The suspension was sonicated on ice for 8 minutes (40% amplitude, 15-second pulse, 10 s interval). The resulting extract was clarified by centrifuging for 40 minutes at 20000 g, 4°C. Ni-Sepharose (GE Healthcare) resin was pre-treated by equilibration with buffer, which was used for preparation of the bacterial cells extract. The resin was then incubated overnight at 4°C with the supernatant obtained after centrifugation of the extract. Then it was loaded into chromatography column and washed with 15 to 50 volumes of buffer 50 mM KH_2PO_4 , 0.5 M NaCl, 20 mM imidazole, pH 7.4. The obtained protein was eluted from the column using imidazole gradient in 50 mM KH_2PO_4 buffer with 0.5 M NaCl, pH 7.4. Obtained fractions were analyzed by SDS-PAGE. Appropriate fractions were combined and dialyzed overnight at 4°C against 50 mM Tris buffer, pH 7.2, 150 mM NaCl, 500 mM L-arginine, 0.1 mM ZnSO_4 , 0.01% Tween 20, and at the same time 10 Histag was cleaved with thrombin (1:50). After the cleavage, thrombin was separated from the target fusion protein using Benzamidine Sepharose™ resin. The purity of the product was analyzed by SDS-PAGE electrophoresis (Maniatis et al, Molecular Cloning. Cold Spring Harbor, NY, 1982).

Overexpression and purification of fusion proteins - general procedure B

LB medium with kanamycin (30 µg/ml) and 100 µM zinc sulfate was inoculated with overnight culture. Cultures were incubated at 37°C until optical density (OD) at 600 nm reached 0.60-0.80. Then IPTG was added to the final concentration in the range 0.5 -1mM. After 20h incubation with shaking at 25°C the culture was centrifuged for 25 min at 6000 g. Bacterial cells after overexpression were disrupted in a French Press in a buffer containing 50 mM KH_2PO_4 , 0.5 M NaCl, 10 mM imidazole, 5mM betamercaptoethanol, 0.5mM PMSF (phenylmethylsulphonyl fluoride), pH 7.8. Resulting extract was clarified by centrifugation for 50 minutes at 8000 g. The obtained supernatant was incubated overnight with Ni-Sepharose resin. Then the resin with bound protein was packed into the chromatography column. To wash-out the fractions containing non-binding proteins, the column was washed with 15 to 50 volumes of buffer 50 mM KH_2PO_4 , 0.5 M NaCl, 10 mM imidazole, 5mM beta-mercaptoethanol, 0.5mM PMSF (phenylmethylsulphonyl fluoride), pH 7.8. Then, to wash-out the majority of proteins binding specifically with the bed, the column was washed with a buffer con-

aining 50 mM KH₂PO₄, 0.5 M NaCl, 500 mM imidazole, 10% glycerol, 0.5mM PMSF, pH 7.5. Obtained fractions were analyzed by SDS-PAGE (Maniatis et al, Molecular Cloning. Cold Spring Harbor, NY, 1982). The fractions containing the target protein were combined and cleaved with thrombin (1U per 4 mg of protein, 8h at 16°C) to remove polyhistidine tag. Then the fractions were dialyzed against formulation buffer (500 mM L-arginine, 50 mM Tris, 2.5 mM ZnSO₄, pH 7.4).

Example 1. The fusion protein of SEQ. No. 1

The protein of SEQ. No. 1 is a fusion protein having the length of 345 amino acids and the mass of 39.8 kDa, in which at the N-terminus of the sequence TRAIL122-281 a 165-amino acid subunit 2b of human interferon alpha (SEQ. No. 17) is attached as an effector peptide. Between the effector peptide and the sequence of TRAIL there are incorporated sequentially next to each other sequences of protease cleavage sites recognized by metalloprotease MMP (SEQ. No. 20) and urokinase uPA (SEQ. No. 21) due to which the effector peptide will undergo cleavage in the tumour environment upon internalization of the fusion protein.

Structure of the fusion protein is shown schematically in Fig. 1 and its amino acid sequence and the DNA encoding sequence comprising codons optimized for expression in *E. coli* are, respectively, SEQ. No. 1 and SEQ. No. 29 as shown in the attached Sequence Listing.

The amino acid sequence SEQ. No. 1 of the structure described above was used as a template to generate its coding DNA sequence SEQ. No. 29. A plasmid containing the coding sequence of DNA was generated and overexpression of the fusion protein was carried out in accordance with the general procedures described above. Overexpression was performed according to the general procedure A, using *E. coli* BL21 (DE3) and *Tuner*(DE3)pLysS strains from Novagen. The protein was separated by electrophoresis in accordance with the general procedure described above.

Example 2. The fusion protein of SEQ. No. 2

The protein of SEQ. No. 2 is a fusion protein having the length of 347 amino acids and the mass of 40 kDa, in which at the C-terminus of the sequence

TRAIL120-281 a 165-amino acid subunit 2b of human interferon alpha (SEQ. No. 17) is attached as an effector peptide. Between the effector peptide and the sequence of TRAIL there are incorporated sequentially next to each other sequences of protease cleavage sites recognized by metalloprotease MMP (SEQ. No. 20) and urokinase uPA (SEQ. No. 21) due to which the effector peptide will undergo cleavage in the tumor environment upon internalization of the fusion protein.

Structure of the fusion protein is shown schematically in Fig. 1 and its amino acid sequence and the DNA encoding sequence comprising codons optimized for expression in *E. coli* are, respectively, SEQ. No. 2 and SEQ. No. 30 as shown in the attached Sequence Listing.

The amino acid sequence SEQ. No. 2 of the structure described above was used as a template to generate its coding DNA sequence SEQ. No. 30. A plasmid containing the coding sequence of DNA was generated and overexpression of the fusion protein was carried out in accordance with the general procedures described above. Overexpression was performed according to the general procedure A, using *E. coli* BL21 (DE3) strain from Novagen. The protein was separated by electrophoresis in accordance with the general procedure described above.

Example 3. The fusion protein of SEQ. No. 3

The protein of SEQ. No. 3 is a fusion protein having the length of 352 amino acids and the mass of 40.4 kDa, in which at the N-terminus of the sequence TRAIL122-281 a 165-amino acid subunit 2b of human interferon alpha (SEQ. No. 17) is attached as an effector peptide. Between the effector peptide and the sequence of TRAIL there are incorporated two combinations of sequences of protease cleavage sites recognized by metalloprotease MMP (SEQ. No. 20) and urokinase uPA (SEQ. No. 21) due to which the effector peptide will undergo cleavage in the tumour environment upon internalization of the fusion protein. Between these two combinations of SEQ. No. 20 and SEQ. No. 21 the fusion protein incorporates additionally linker for pegylation (SEQ. No. 22).

Structure of the fusion protein is shown schematically in Fig. 1 and its amino acid sequence and the DNA encoding sequence comprising codons optimized for

expression in *E. coli* are, respectively, SEQ. No. 3 and SEQ. No. 31 as shown in the attached Sequence Listing.

The amino acid sequence SEQ. No. 3 presented above was used as a template to generate its coding DNA sequence SEQ. No 31 presented above. A plasmid containing the coding sequence of DNA was generated and overexpression of the fusion protein was carried out in accordance with the general procedures described above. Overexpression was performed according to the general procedure B, using *E.coli* strain BL21 (DE3) from Novagen. The protein was separated by electrophoresis in accordance with the general procedure described above.

Example 4. The fusion protein of SEQ. No. 4

The protein of SEQ. No. 4 is a fusion protein having the length of 353 amino acids and the mass of 40.5 kDa, in which at the C-terminus of the sequence TRAIL121-281 a 165-amino acid subunit 2b of human interferon alpha (SEQ. No. 17) is attached as an effector peptide. Between the effector peptide and the sequence of TRAIL there are incorporated two combinations of sequences of protease cleavage sites recognized by metalloprotease MMP (SEQ. No. 20) and urokinase uPA (SEQ. No. 21) due to which the effector peptide will undergo cleavage in the tumour environment upon internalization of the fusion protein. Between these two combinations of SEQ. No. 20 and SEQ. No. 21 the fusion protein incorporates additionally the linker for pegylation (SEQ. No. 22).

Structure of the fusion protein is shown schematically in Fig. 1 and its amino acid sequence and the DNA encoding sequence comprising codons optimized for expression in *E. coli* are, respectively, SEQ. No. 4 and SEQ. No. 32 as shown in the attached Sequence Listing.

The amino acid sequence SEQ. No. 4 presented above was used as a template to generate its coding DNA sequence SEQ. No 32 presented above. A plasmid containing the coding sequence of DNA was generated and overexpression of the fusion protein was carried out in accordance with the general procedures described above. Overexpression was performed according to the general procedure B, using *E. coli* BL21DE3pLysSRIL strain from Stratagene and *E. coli* Tuner (DE3) z from Novagen. The protein was separated by electrophoresis in accordance with the general procedure described above.

Example 5. The fusion protein of SEQ. No. 5

The protein of SEQ. No. 5 is a fusion protein having the length of 300 amino acids and the mass of 34.7 kDa, in which at the N-terminus of the sequence TRAIL116-281 a fragment of human interferon gamma (SEQ. No. 18) is attached as an effector peptide. Between the effector peptide and the sequence of TRAIL the protein contains sequences of protease cleavage sites recognized by metalloprotease MMP (SEQ. No. 20) and urokinase uPA (SEQ. No. 21).

Structure of the fusion protein is shown schematically in Fig. 2 and its amino acid sequence and the DNA encoding sequence comprising codons optimized for expression in *E. coli* are, respectively, SEQ. No. 5 and SEQ. No. 33 as shown in the attached Sequence Listing.

The amino acid sequence SEQ. No. 5 of the structure described above was used as a template to generate its coding DNA sequence SEQ. No. 33. A plasmid containing the coding sequence of DNA was generated and overexpression of the fusion protein was carried out in accordance with the general procedures described above. Overexpression was performed according to the general procedure A, using *E. coli Tuner (DE3)* strain from Novagen. The protein was separated by electrophoresis in accordance with the general procedure described above.

Example 6. The fusion protein of SEQ. No. 6

The protein of SEQ. No. 6 is a fusion protein having the length of 307 amino acids and the mass of 35.1 kDa, in which at the C-terminus of the sequence TRAIL116-281 a fragment of human interferon gamma (SEQ. No. 18) is attached as an effector peptide. Between the effector peptide and the sequence of TRAIL the protein contains sequences of protease cleavage sites recognized by metalloprotease MMP (SEQ. No. 20) and urokinase uPA (SEQ. No. 21).

The protein comprises also flexible linkers: flexible glycine-serine linker (SEQ. No. 27) between the sequence of TRAIL and metalloprotease MMP cleavage site; and flexible glycine-serine linker (SEQ. No. 28) between the urokinase uPa cleavage site and the effector sequence.

Structure of the fusion protein is shown schematically in Fig. 2 and its amino acid sequence and the DNA encoding sequence comprising codons optimized for

expression in *E. coli* are, respectively, SEQ. No. 6 and SEQ. No. 34 as shown in the attached Sequence Listing.

The amino acid sequence SEQ. No. 6 of the structure described above was used as a template to generate its coding DNA sequence SEQ. No. 34. A plasmid
5 containing the coding sequence of DNA was generated and overexpression of the fusion protein was carried out in accordance with the general procedures described above. Overexpression was performed according to the general procedure A, using *E. coli Tuner(DE3)* strain from Novagen. The protein was separated by electrophoresis in accordance with the general procedure described above.

10 Example 7. The fusion protein of SEQ. No. 7

The protein of SEQ. No. 7 is a fusion protein having the length of 310 amino acids and the mass of 35.5 kDa, in which at the N-terminus of the sequence TRAIL116-281 a fragment of human interferon gamma (SEQ. No. 18) is attached as an effector peptide. Between the effector peptide and the sequence of TRAIL
15 the protein contains sequences of protease cleavage sites recognized by metalloprotease MMP (SEQ. No. 20) and urokinase uPA (SEQ. No. 21).

The protein comprises also flexible linkers: flexible glycine-serine linker of SEQ. No. 26 between the sequence of effector peptide and metalloprotease MMP cleavage site; and flexible glycine-serine linker SEQ. No. 26 between the
20 urokinase uPa cleavage site and TRAIL sequence.

Structure of the fusion protein is shown schematically in Fig. 2 and its amino acid sequence and the DNA encoding sequence comprising codons optimized for expression in *E. coli* are, respectively, SEQ. No. 7 and SEQ. No. 35 as shown in the attached Sequence Listing.

25 The amino acid sequence SEQ. No. 7 of the structure described above was used as a template to generate its coding DNA sequence SEQ. No. 35. A plasmid containing the coding sequence of DNA was generated and overexpression of the fusion protein was carried out in accordance with the general procedures described above. Overexpression was performed according to the general
30 procedure A, using *E. coli Tuner(DE3)* strain from Novagen. The protein was separated by electrophoresis in accordance with the general procedure described above.

Example 8. The fusion protein of SEQ. No. 8

The protein of SEQ. No. 8 is a fusion protein having the length of 310 amino acids and the mass of 35.3 kDa, in which at the C-terminus of the sequence TRAIL116-281 a fragment of human interferon gamma (SEQ. No. 18) is attached
5 as an effector peptide. Between the effector peptide and the sequence of TRAIL the protein contains sequences of protease cleavage sites recognized by metalloprotease MMP (SEQ. No. 20) and urokinase uPA (SEQ. No. 21).

The protein comprises also flexible linkers: flexible glycine-serine linker GSGGG (SEQ. No. 26) between the sequence of effector peptide and metalloprotease
10 MMP cleavage site; and flexible glycine-serine linker GSGGG (SEQ. No. 26) between the urokinase uPa cleavage site and TRAIL sequence.

Structure of the fusion protein is shown schematically in Fig. 2 and its amino acid sequence and the DNA encoding sequence comprising codons optimized for expression in *E. coli* are, respectively, SEQ. No. 8 and SEQ. No. 36 as shown in
15 the attached Sequence Listing.

The amino acid sequence SEQ. No. 8 of the structure described above was used as a template to generate its coding DNA sequence SEQ. No. 36. A plasmid containing the coding sequence of DNA was generated and overexpression of the fusion protein was carried out in accordance with the general procedures
20 described above. Overexpression was performed according to the general procedure A, using *E. coli Tuner(DE3)* strain from Novagen. The protein was separated by electrophoresis in accordance with the general procedure described above

Example 9. The fusion protein of SEQ. No. 9

25 The protein of SEQ. No. 9 is a fusion protein having the length of 317 amino acids and the mass of 35.9 kDa, in which at the N-terminus of the sequence TRAIL116-281 a fragment of human interferon gamma (SEQ. No. 18) is attached as an effector peptide. Between the effector peptide and the sequence of TRAIL there is incorporated the combination of protease cleavage sites recognized by
30 metalloprotease MMP (SEQ. No. 20) and urokinase uPA (SEQ. No. 21) due to which the effector peptide will undergo cleavage in the tumour environment upon internalization of the fusion protein. Between the SEQ. No. 20 and SEQ.

No. 21 the fusion protein contains additionally the linker for pegylation (SEQ. No. 22).

The protein comprises also flexible linkers: flexible glycine-serine linker GSGGG (SEQ. No. 26) between the sequence of effector peptide and metalloprotease
5 MMP cleavage site; and flexible glycine-serine linker GSGGG (SEQ. No. 26) between the urokinase uPa cleavage site and TRAIL sequence.

Structure of the fusion protein is shown schematically in Fig. 2 and its amino acid sequence and the DNA encoding sequence comprising codons optimized for expression in *E. coli* are, respectively, SEQ. No. 9 and SEQ. No. 37 as shown in
10 the attached Sequence Listing.

The amino acid sequence SEQ. No. 9 of the structure described above was used as a template to generate its coding DNA sequence SEQ. No. 37. A plasmid containing the coding sequence of DNA was generated and overexpression of the fusion protein was carried out in accordance with the general procedures
15 described above. Overexpression was performed according to the general procedure A, using *E. coli* Rosetta (DE3) strain from Novagen. The protein was separated by electrophoresis in accordance with the general procedure described above.

Example 10. The fusion protein of SEQ. No. 10

20 The protein of SEQ. No. 10 is a fusion protein having the length of 338 amino acids and the mass of 38.3 kDa, in which at the N-terminus of the sequence TRAIL95-281 a fragment of human interferon gamma (SEQ. No. 18) is attached as an effector peptide. Between the effector peptide and the sequence of TRAIL the fusion protein contains the sequences of protease cleavage sites recognized
25 by metalloprotease MMP (SEQ. No. 20) and urokinase uPA (SEQ. No. 21) due to which the effector peptide will undergo cleavage in the tumor environment upon internalization of the fusion protein. Next to the SEQ. No. 21 the fusion protein contains additionally the linker for pegylation (SEQ. No. 22).

The protein comprises also flexible linkers: between the sequence of effector peptide and metalloprotease MMP cleavage site the flexible glycine-serine linker
30 GSGGG (SEQ. No. 26); and between the linker for pegylation and TRAIL sequence the flexible glycine-serine linker GSGGG (SEQ. No. 26).

Structure of the fusion protein is shown schematically in Fig. 2 and its amino acid sequence and the DNA encoding sequence comprising codons optimized for expression in *E. coli* are, respectively, SEQ. No. 10 and SEQ. No. 38 as shown in the attached Sequence Listing.

- 5 The amino acid sequence SEQ. No. 10 of the structure described above was used as a template to generate its coding DNA sequence SEQ. No. 38. A plasmid containing the coding sequence of DNA was generated and overexpression of the fusion protein was carried out in accordance with the general procedures described above. Overexpression was performed according to the general
10 procedure A, using *E. coli* BL21 (DE3) and *Tuner(DE3)pLysS* strains from Novagen. The protein was separated by electrophoresis in accordance with the general procedure described above.

Example 11. The fusion protein of SEQ. No. 11

- The protein of SEQ. No. 11 is a fusion protein having the length of 317 amino
15 acids and the mass of 35.9 kDa, in which at the C-terminus of the sequence TRAIL116-281 a fragment of human interferon gamma (SEQ. No. 18) is attached as an effector peptide. Between the effector peptide and the sequence of TRAIL the protein contains sequences of protease cleavage sites recognized by metalloprotease MMP (SEQ. No. 20) and urokinase uPA (SEQ. No. 21) due to
20 which the effector peptide will undergo cleavage in the tumour environment upon internalization of the fusion protein. Between SEQ. No. 20 and SEQ. No. 21 the fusion protein contains additionally linker for pegylation (SEQ. No. 22).

- The protein comprises also flexible linkers: flexible glycine-serine linker GSGGG (SEQ. No. 26) between the sequence of effector peptide and metalloprotease
25 MMP cleavage site; and flexible glycine-serine linker GSGGG (SEQ. No. 26) between the urokinase uPa cleavage site and TRAIL sequence.

- Structure of the fusion protein is shown schematically in Fig. 2 and its amino acid sequence and the DNA encoding sequence comprising codons optimized for expression in *E. coli* are, respectively, SEQ. No. 11 and SEQ. No. 39 as shown in
30 the attached Sequence Listing.

The amino acid sequence SEQ. No. 11 of the structure described above was used as a template to generate its coding DNA sequence SEQ. No. 39. A plasmid containing the coding sequence of DNA was generated and overexpression of the fusion protein was carried out in accordance with the general procedures

described above. Overexpression was performed according to the general procedure A, using *E. coli* BL21 (DE3) and *E. coli* Tuner(DE3)pLysS strains from Novagen. The protein was separated by electrophoresis in accordance with the general procedure described above.

5 Example 12. The fusion protein of SEQ. No. 12

The protein of SEQ. No. 12 is a fusion protein having the length of 449 amino acids and the mass of 51.8 kDa, in which at the N-terminus of the sequence TRAIL116-281 a single chain pseudodimer of human interferon gamma (SEQ. No. 19) is attached as an effector peptide. Between the effector peptide and the
10 sequence of TRAIL the protein contains sequences of protease cleavage sites recognized by metalloprotease MMP (SEQ. No. 20) and urokinase uPA (SEQ. No. 21) due to which the effector peptide will undergo cleavage in the tumour environment upon internalization of the fusion protein.

The protein comprises also flexible linkers: flexible glycine-serine linker GSGGG
15 (SEQ. No. 26) between the sequence of effector peptide and metalloprotease MMP cleavage site; and flexible glycine-serine linker GSGGG (SEQ. No. 26) between the urokinase uPa cleavage site and TRAIL sequence.

Structure of the fusion protein is shown schematically in Fig. 3 and its amino acid sequence and the DNA encoding sequence comprising codons optimized for
20 expression in *E. coli* are, respectively, SEQ. No. 12 and SEQ. No. 40 as shown in the attached Sequence Listing.

The amino acid sequence SEQ. No. 12 of the structure described above was used as a template to generate its coding DNA sequence SEQ. No. 40. A plasmid containing the coding sequence of DNA was generated and overexpression of the
25 fusion protein was carried out in accordance with the general procedures described above. Overexpression was performed according to the general procedure A, using *E. coli* BL21 (DE3) and *E. coli* Tuner(DE3)pLysS strains from Novagen. The protein was separated by electrophoresis in accordance with the general procedure described above.

30 Example 13. The fusion protein of SEQ. No. 13

The protein of SEQ. No. 13 is a fusion protein having the length of 449 amino acids and the mass of 51.8 kDa, in which at the C-terminus of the sequence TRAIL116-281 a single chain pseudodimer of human interferon gamma (SEQ. No. 19) is attached as an effector peptide. Between the effector peptide and the

sequence of TRAIL there are incorporated sequentially sequences of protease cleavage sites recognized by metalloprotease MMP (SEQ. No. 20) and urokinase uPA (SEQ. No. 21) due to which the effector peptide will undergo cleavage in the tumor environment upon internalization of the fusion protein.

- 5 The protein comprises also flexible linkers: flexible glycine-serine linker GSGGG (SEQ. No. 26) between the sequence of effector peptide and urokinase uPA cleavage site; and flexible glycine-serine linker GSGGG (SEQ. No. 26) between the metalloprotease MMP cleavage site and TRAIL sequence.

Structure of the fusion protein is shown schematically in Fig. 3 and its amino
10 acid sequence and the DNA encoding sequence comprising codons optimized for expression in *E. coli* are, respectively, SEQ. No. 13 and SEQ. No. 41 as shown in the attached Sequence Listing.

The amino acid sequence SEQ. No. 13 presented above was used as a template to generate its coding DNA sequence SEQ. No 41 presented above. A plasmid
15 containing the coding sequence of DNA was generated and overexpression of the fusion protein was carried out in accordance with the general procedures described above. Overexpression was performed according to the general procedure B, using *E. coli* B.21 (DE3) strain from Novagen and *E. coli* L21DE3pLysSRIL strain from Stratagene. The protein was separated by
20 electrophoresis in accordance with the general procedure described above.

Example 14. The fusion protein of SEQ. No. 14

The protein of SEQ. No. 14 is a fusion protein having the length of 456 amino acids and the mass of 52.4 kDa, in which at the N-terminus of the sequence
25 TRAIL116-281 a single chain pseudodimer of human interferon gamma (SEQ. No. 19) is attached as an effector peptide. Between the effector peptide and the sequence of TRAIL there are incorporated sequences of protease cleavage sites recognized by metalloprotease MMP (SEQ. No. 20) and urokinase uPA (SEQ. No. 21) due to which the effector peptide will undergo cleavage in the tumour environment upon internalization of the fusion protein. Between the sequences
30 SEQ. No. 20 and SEQ. No. 21 the fusion protein contains additionally linker for pegylation (SEQ. No. 22).

The protein comprises also flexible linkers: flexible glycine-serine linker GSGGG

(SEQ. No. 26) between the sequence of effector peptide and urokinase uPa cleavage site; and flexible glycine-serine linker GSGGG (SEQ. No. 26) between the metalloprotease MMP cleavage site and TRAIL sequence.

Structure of the fusion protein is shown schematically in Fig. 3 and its amino acid sequence and the DNA encoding sequence comprising codons optimized for expression in *E. coli* are, respectively, SEQ. No. 14 and SEQ. No. 42 as shown in the attached Sequence Listing.

The amino acid sequence SEQ. No. 14 presented above was used as a template to generate its coding DNA sequence SEQ. No. 42 presented above. A plasmid containing the coding sequence of DNA was generated and overexpression of the fusion protein was carried out in accordance with the general procedures described above. Overexpression was performed according to the general procedure B, using *E. coli* B.21 (DE3) strain from Novagen and *E. coli* BL21DE3pLysSRIL strain from Stratagene. The protein was separated by electrophoresis in accordance with the general procedure described above.

Example 15. The fusion protein of SEQ. No. 15

The protein of SEQ. No. 15 is a fusion protein having the length of 456 amino acids and the mass of 52.4 kDa, in which at the C-terminus of the sequence TRAIL116-281 a single chain pseudodimer of human interferon gamma (SEQ. No. 19) is attached as an effector peptide. Between the sequence of TRAIL and the effector peptide the fusion protein contains sequences of protease cleavage sites recognized by metalloprotease MMP (SEQ. No. 20) and urokinase uPA (SEQ. No. 21) due to which the effector peptide will undergo cleavage in the tumour environment upon internalization of the fusion protein. Between the sequences SEQ. No. 20 and SEQ. No. 21 the fusion protein contains additionally the linker for pegylation (SEQ. No. 22).

The protein comprises also flexible linkers: flexible glycine-serine linker GSGGG (SEQ. No. 26) between the sequence of effector peptide and urokinase uPa cleavage site; and flexible glycine-serine linker GSGGG (SEQ. No. 26) between the sequence of TRAIL and the metalloprotease MMP cleavage site.

Structure of the fusion protein is shown schematically in Fig. 3 and its amino acid sequence and the DNA encoding sequence comprising codons optimized for expression in *E. coli* are, respectively, SEQ. No. 15 and SEQ. No. 43 as shown in

the attached Sequence Listing.

The amino acid sequence SEQ. No. 15 presented above was used as a template to generate its coding DNA sequence SEQ. No. 43 presented above. A plasmid containing the coding sequence of DNA was generated and overexpression of the fusion protein was carried out in accordance with the general procedures described above. Overexpression was performed according to the general procedure B, using *E. coli* B.21 (DE3) strain from Novagen and *E. coli* L21DE3pLysSRIL strain from Stratagene. The protein was separated by electrophoresis in accordance with the general procedure described above.

Example 16. The fusion protein of SEQ. No. 44

The protein of SEQ. No. 44 is a fusion protein having the length of 538 amino acids and the mass of 62,4 kDa, in which at the N-terminus of the sequence TRAIL122-281 a single chain pseudodimer of human interferon alpha 2b (SEQ. No. 46) is attached as an effector peptide. Between the sequence of the effector peptide and the sequence of TRAIL there are incorporated two combinations of sequences of protease cleavage sites recognized by metalloprotease MMP (SEQ. No. 20) and urokinase uPA (SEQ. No. 21) due to which the effector peptide will undergo cleavage in the tumour environment upon internalization of the fusion protein. Between the two combinations of sequences SEQ. No. 20 and SEQ. No. 21 the fusion protein contains additionally linker for pegylation (SEQ. No. 22).

Structure of the fusion protein is shown schematically in Fig. 4 and its amino acid sequence and the DNA encoding sequence comprising codons optimized for expression in *E. coli* are, respectively, SEQ. No. 44 and SEQ. No. 48 as shown in the attached Sequence Listing.

The amino acid sequence SEQ. No. 44 presented above is used as a template to generate its coding DNA sequence SEQ. No. 48 presented above. A plasmid containing the coding sequence of DNA can be generated and overexpression of the fusion protein carried out in accordance with the general procedures described above. Overexpression can be performed according to the general procedure B, using *E. coli* B.21 (DE3) strain from Novagen and *E. coli* L21DE3pLysSRIL strain from Stratagene. The protein can be separated by electrophoresis in accordance with the general procedure described above.

Example 17. The fusion protein of SEQ. No. 45

The protein of SEQ. No. 45 is a fusion protein having the length of 384 amino acids and the mass of 44 kDa, in which at the N-terminus of the sequence TRAIL95-281 a consensus sequence of human interferon alpha (SEQ. No. 47) is attached as an effector peptide. Between the sequence of the effector peptide and the sequence of TRAIL there are incorporated two combinations of sequences of protease cleavage sites recognized by metalloprotease MMP (SEQ. No. 20) and urokinase uPA (SEQ. No. 21) due to which the effector peptide will undergo cleavage in the tumour environment upon internalization of the fusion protein. Between the combinations of sequences SEQ. No. 20 and SEQ. No. 21 the fusion protein contains additionally linker for pegylation (SEQ. No. 22). The protein comprises also flexible glycine-serine linker GGSG (SEQ. No. 50) between the sequence of effector peptide and metalloprotease MMP cleavage site.

Structure of the fusion protein is shown schematically in Fig. 4 and its amino acid sequence and the DNA encoding sequence comprising codons optimized for expression in *E. coli* are, respectively, SEQ. No. 45 and SEQ. No. 49 as shown in the attached Sequence Listing.

The amino acid sequence SEQ. No. 45 presented above is used as a template to generate its coding DNA sequence SEQ. No 49 presented above. A plasmid containing the coding sequence of DNA can be generated and overexpression of the fusion protein carried out in accordance with the general procedures described above. Overexpression can be performed according to the general procedure B, using *E. coli* B.21 (DE3) strain from Novagen and *E. coli* L21DE3pLysSRIL strain from Stratagene. The protein can separated by electrophoresis in accordance with the general procedure described above.

Example 18. Examination of anti-tumor activity of the fusion proteins

Examination of anti-tumor activity of the fusion proteins was carried out *in vitro* in a cytotoxicity assay on tumor cell lines and *in vivo* in mice. For comparison purposes, rhTRAIL114-281 protein and placebo were used.

1. Measurement of circular dichroism

Quality of the preparations of fusion proteins in terms of their structure was determined by circular dichroism (CD) for Ex. 3, Ex. 5, Ex. 12 and Ex. 14.

Circular dichroism is used for determination of secondary structures and conformation of protein. CD method uses optical activity of the protein structures, manifested in rotating the plane of polarization of light and the

appearance of elliptical polarization. CD spectrum of proteins in far ultraviolet (UV) provides precise data on the conformation of the main polypeptide chain.

Samples of the protein to be analysed after formulation into a buffer consisting of 50 mM Tris-HCl pH 8.0, 100 mM NaCl, 10% glycerol, 0.1 mM ZnCl₂, 80 mM
5 saccharose, 5mM DTT were dialysed in the dialysis bags (Sigma-Aldrich) with cut off 12 kDa. Dialysis was performed against 100 fold excess (v/v) of buffer comparing to the protein preparations with stirring for several hours at 4°C. After dialysis was completed, each preparation was centrifuged (25 000 rpm, 10 min., 4°C) and the appropriate supernatants were collected. Protein
10 concentration in the samples thus obtained was determined by Bradford method.

Measurement of circular dichroism for proteins in the concentration range of 0,1-2,7 mg/ml was performed on Jasco J-710 spectropolarimeter, in a quartz cuvette with optical way 0.2 mm or 1 mm. The measurement was performed under the flow of nitrogen at 7 l/min, which allowed to perform of the measure-
15 ment in the wavelength range from 195 to 250 nm. Parameters of the measurement: spectral resolution of - 1 nm; half width of the light beam 1 nm; sensitivity 20 mdeg, the averaging time for one wavelength - 8 s, scan speed 10 nm/min.

The results were presented as the average of three measurements. Circular dichroism spectra for rhTRAIL114-281, rhTRAIL95-281 and proteins of Ex. 12, Ex.
20 5, Ex. 3 and Ex. 14 are presented in Fig. 5.

Obtained spectra were analyzed numerically in the range of 193-250 nm using CDPro software. Points for which the voltage at the photomultiplier exceeded 700 V were omitted, due to too low signal to noise ratio in this wavelength range.

25 The data obtained served for calculations of particular secondary structures content in the analyzed proteins with use of CDPro software (Table 1).

Table 1. Content of secondary structures in the analyzed proteins

Protein	NRMSD (Exp-Cal)	α -helix	β - sheet	Schift	Disorder
Ex. 3	0.018	98.0%	1.5%	0.0%	0.5%
Ex. 5	0.048	45.6%	8.2%	18.8%	27.4%
Ex.12	0.104	39.3%	17.3%	15.0%	28.4%
Ex. 14	0.01	100.0%	0.0%	0.0%	0.0%
hrTRAIL*		1.94%	50.97%	7.74%	39.35%
hrTRAIL114-281	0.389	4.9%	33.7%	23.1%	38.3%
hrTRAIL 95	0.074	0.0%	21.6%	16.0%	62.4%

* value obtained on the basis of crystalline structure 1D4V

Controls (rhTRAIL114-281 and rhTRAIL95-281) show CD spectrum characteristic for the proteins with predominantly type β -sheet structures (sharply outlined ellipticity minimum at the wavelength 220 nm). This confirms the calculation of secondary structure components, which suggests a marginal number of α -helix elements.

The obtained result is also consistent with data from the crystal structure of TRAIL protein, wherein beta elements constitute more than half of its composition.

In the case of fused proteins of Ex. 3, Ex. 5, Ex. 12 and Ex. 14, dichroism spectra are characterized by two minima at wavelengths 208 and 220 nm, which is characteristic for proteins with mixed secondary structure of alpha/beta type.

Interferon molecules attached to TRAIL in the fused proteins form predominantly alpha-helical structures, therefore the mixed nature of secondary structures in the analyzed chimeric proteins can confirm the presence of properly folded elements of both TRAIL and interferon.

In the case of preparations according to Ex. 3. and Ex. 14, almost 100% of alpha-type structures was found. Such a content of alpha type structures is due to narrow range of wavelength used in analysis, which is a consequence of the selection of formulations optimal for methods and materials (high amount of noise in the far-UV). The absence of sharply outlined range of 180-200 nm in the analyzed region of the spectrum can cause that content of α -helix structures is over-estimated.

2. Tests on cell lines *in vitro*Cell lines

Table 2. Adherent cell lines

Cell line	Cancer type	Medium	number of cells per well (thousands)
Colo 205 ATCC #CCL-222	<i>human colorectal cancer</i>	RPMI + 10% FBS + penicillin + streptomycin	5
HT-29 ATCC # CCL-2	<i>human colorectal cancer</i>	McCoy's + 10% FBS + penicillin + streptomycin	5
DU-145 ATCC # HTB-81	<i>human prostate cancer</i>	RPMI + 10% FBS + penicillin + streptomycin	3
PC-3 ATCC # CRL-1435	<i>human prostate cancer</i>	RPMI + 10% FBS + penicillin + streptomycin	4
MCF-7 ATCC #HTB-22	<i>human breast cancer</i>	MEM + 10% FBS + penicillin + streptomycin	4,5
MDA-MB-231 ATCC # HTB-26	<i>human breast cancer</i>	DMEM + 10% FBS + penicillin + streptomycin	4,5
UM-UC-3 ATCC # CLR-1749	<i>human bladder cancer</i>	MEM + 10% FBS + penicillin + streptomycin	3,5
SW780 ATCC #CRL-2169	<i>human bladder cancer</i>	DMEM + 10% FBS + penicillin + streptomycin	3
SW620 ATCC #CCL-227	<i>human colorectal cancer</i>	DMEM + 10% FBS + penicillin + streptomycin	5
BxPC-3 ATCC #CRL-1687	<i>human pancreatic cancer</i>	RPMI + 10% FBS + penicillin + streptomycin	4,5
SK-OV-3 ATCC # HTB-77	<i>human ovarian cancer</i>	McCoy's + 10% FBS + penicillin + streptomycin	4
NIH: OVCAR-3 ATCC #HTB-161	<i>human ovarian cancer</i>	RPMI + 20% FBS + 0,01mg/ml insulin + penicillin + streptomycin	7
HepG2 ATCC # HB-8065	<i>human liver hepatoma</i>	MEM + 10% FBS + penicillin + streptomycin	7
293 ATCC # CLR-1573	<i>Human embrional kidney cells</i>	MEM + 10% FBS + penicillin + streptomycin	4
ACHN ATCC #CCL-222	<i>human kidney cancer</i>	MEM + 10% FBS + penicillin + streptomycin	4
CAKI 2 ATCC # HTB-47	<i>human kidney cancer</i>	McCoy's + 10% FBS + penicillin + streptomycin	3,5
NCI- H69AR ATCC #CRL-11351	<i>human small cell lung cancer</i>	RPMI + 10% FBS + penicillin + streptomycin	10
HT144 ATCC # HTB-63	<i>human melanoma cells</i>	McCoy's + 10% FBS + penicillin + streptomycin	7
NCI-H460 ATCC #HTB-177	<i>human lung cancer</i>	MEM + 10% FBS + penicillin + streptomycin	2,5
LNCaP ATCC # CRL-1740	<i>human prostate cancer</i>	RPMI + 10% FBS + penicillin + streptomycin	4,5

Table 3. Nonadherent cells:

Cell line	Cancer type	Medium	Number of cells per well (thousands)
NCI-H69 ATCC# HTB-119	human small cell lung cancer	RPMI + 10% FBS + penicillin + streptomycin	22
Jurkat A3 ATCC#CRL-2570	<i>human leukaemia</i>	RPMI + 10% FBS + penicillin + streptomycin	10
HL60 ATCC# CCL-240	<i>human leukaemia</i>	RPMI + 20% FBS + penicillin + streptomycin	10
CCRF-CEM ATCC# CCL-119	<i>human leukaemia</i>	RPMI + 20% FBS + penicillin + streptomycin	10

MTT cytotoxicity test

MTT assay is a colorimetric assay used to measure proliferation, viability and cytotoxicity of cells. It consists in decomposition of a yellow tetrazolium salt MTT (4,5-dimethyl-2-thiazolyl)-2,5-diphenyltetrazolium bromide) to the water-insoluble purple dye formazan by mitochondrial enzyme succinate-tetrazolium reductase 1. MTT reduction occurs only in living cells. Data analysis consists in determining IC₅₀ concentration of the protein (in ng/ml), at which the 50% reduction in the number of cells occurs in the population treated compared to control cells. Results were analyzed using GraphPad Prism 5.0 software. The test was performed according to the literature descriptions (Celis, JE, (1998). Cell Biology, a Laboratory Handbook, second edition, Academic Press, San Diego; Yang, Y., Koh, LW, Tsai, JH., (2004); Involvement of viral and chemical factors with oral cancer in Taiwan, Jpn J Clin Oncol, 34 (4), 176-183).

Cell culture medium was diluted to a defined density (10^4 - 10^5 cells per 100 μ l). Then 100 μ l of appropriately diluted cell suspension was applied to a 96-well plate in triplicates. Thus prepared cells were incubated for 24 h at 37°C in 5% or 10% CO₂, depending on the medium used, and then to the cells (in 100 μ l of medium) further 100 μ l of the medium containing various concentrations of tested proteins were added. After incubation of the cells with tested proteins over the period of next 72 hours, which is equivalent to 3-4 times of cell division, the medium with the test protein was added with 20 ml of MTT working solution [5 mg/ml], and incubation was continued for 3 h at 37°C in 5% CO₂.

Then the medium with MTT solution was removed, and formazan crystals were dissolved by adding 100 μ l of DMSO. After stirring, the absorbance was measured at 570 nm (reference filter 690 nm).

EZ4U cytotoxicity test

EZ4U (Biomedica) test was used for testing cytotoxic activity of the proteins in nonadherent cell lines. The test is a modification of the MTT wherein formazan formed in the reduction of tetrazolium salt is water-soluble. Cell viability study
5 was carried out after continuous 72-hour incubation of the cells with protein (seven concentrations of protein, each in triplicates). On this basis IC₅₀ values were determined (as an average of two independent experiments) using the GraphPad Prism 5 software.

The results of *in vitro* cytotoxicity tests are summarized in Table 4 and Table 5,
10 as IC₅₀ values (ng/ml), which corresponds to a protein concentration at which the cytotoxic effect of fusion proteins is observed at the level of 50% with respect to control cells treated only with solvent. Each experiment represents the average value of at least two independent experiments performed in triplicates. As a criterion of lack of activity of protein preparations the IC₅₀ limit
15 of 2000 ng/ml was adopted. Fusion proteins with an IC₅₀ value above 2000 were considered inactive.

Cells for this test were selected so as to include the tumor cell lines naturally resistant to TRAIL protein (the criterion of natural resistance to TRAIL: IC₅₀ for TRAIL protein > 2000), tumor cell lines sensitive to TRAIL protein and resistant to
20 doxorubicin line MES-SA/DX5 as a cancer line resistant to conventional anticancer medicaments.

Undifferentiated HUVEC cell line was used as a healthy control cell line for assessment of the effect/toxicity of the fusion proteins in non-cancer cells.

The results obtained confirm the possibility of overcoming the resistance of the
25 cell lines to TRAIL by administration of certain fusion proteins of the invention to cells naturally resistant to TRAIL. When fusion proteins of the invention into the cells sensitive to TRAIL were administered, in some cases a clear and strong potentiation of the potency of action was observed, manifesting in reduced IC₅₀ values of the fusion protein compared with IC₅₀ for the TRAIL alone.
30 Furthermore, cytotoxic activity of the fusion protein of the invention in the cells resistant to classical anti-cancer medicament doxorubicin was obtained, and in some cases was stronger than activity of TRAIL alone.

The IC_{50} values above 2000 obtained for the non-cancer cell lines show the absence of toxic effects associated with the use of proteins of the invention for healthy cells, which indicates potential low systemic toxicity of the protein.

Determination of cytotoxic activity of selected protein preparations against
5 extended panel of tumour cell lines

Table 5 presents the results of the tests of cytotoxic activity *in vitro* for selected fusion proteins of the invention against a broad panel of tumour cells from different organs, corresponding to the broad range of most common cancers. Obtained IC_{50} values confirm high cytotoxic activity of fusion proteins and thus
10 their potential utility in the treatment of cancer.

Table 4. Cytotoxic activity of fusion proteins of the invention

Protein	Continuous incubation of preparations with cells over 72h (MTT test, ng/ml)											
	MES-SA		MES-SA/Dx5		HCT116		SK-MES-1		A549		MCF10A	
	IC ₅₀	±SD	IC ₅₀	±SD	IC ₅₀	±SD	IC ₅₀	±SD	IC ₅₀	±SD	IC ₅₀	±SD
rhTRAIL95-281	>2000		32.2	2.40	173	31.3	12.2	2.33	>2000		>2000	
Ex. 1	196.5	11.74	46.9	0.16	210.7	102.67	108.2	28.43	>2000		>2000	
Ex. 3	68.31	3.5	26.54	5.2	37.97	1.9	17.91	34.1	872.2	85.3	>2000	
Ex. 5	57.18	40.8	14.11	6.7	72.1	36.1	53.84	30.9	1326	888.2	>2000	
Ex. 12	1.33	0.54	2.73	2.23	1.90	0.22	1.82	1.00	526	107.4	>2000	
Ex. 14	0.09	0.01	0.059	0.08	2.10	0.33	0.06	0.01	672.80	8.20	>2000	

Table 5. Analysis of cytotoxic activity of selected protein preparations against broad panel of tumour cell lines

Cell line	COLO 205		HT 29		SW 620		MCF 7		MDA-MB-231		DU 145		LNCaP		PC 3	
	mean	SD	mean	SD	mean	SD	mean	SD	mean	SD	mean	SD	mean	SD	mean	SD
rhTRAIL95-281	24.9	17.68	10000		10000		10000		10000		10000		2052	466.0	10000	
Ex. 14	2.916	0.70	131.5	33.23	562.5	371.7	3901	2745.7	6.38	3.21	34.75	12.37	1378	377.60	1325	
Cell line	SW 780		UM-UC-3		293		CAKI 2		SK-OV-3		OV-CAR-3		H69AR		NCI-H69	
	mean	SD	mean	SD	mean	SD	mean	SD	mean	SD	mean	SD	mean	SD	mean	SD
rhTRAIL95-281	120	42.43	2242	1367	10000		10000		10000		93.1	8.34	10000		10000	
Ex. 14	0.766	1.04	3.154	0.21	10000	0.0	6594	3661.4	8172	2585.9	0.007	0.01	3889	864.79	10000	
Cell line	NCI-H460		BxPC3		HepG2		HT 144		ACHN		JURKAT A3		HL60		CCRF-CEM	
	mean	SD	mean	SD	mean	SD	mean	SD	mean	SD	mean	SD	mean	SD	mean	SD
rhTRAIL95-281	5889	111.0	64.71	31.81	10000		1734	218.5	10000		10000		10000		10000	
Ex. 14	0.547	0.25	0.137	0.11	10000	0.00	0.13	0.02	2.95	1.29	0.112	0.1	10000		10000	
Cell line	COLO 205		HT 29		SW 620		MCF 7		MDA-MB-231		DU 145		LNCaP		PC 3	
	mean	SD	mean	SD	mean	SD	mean	SD	mean	SD	mean	SD	mean	SD	mean	SD
rhTRAIL95-281	24.9	17.68	10000		10000		10000		10000		10000		2052	466.0	10000	
Ex. 5	5.717	1.69	159.6	7.64	683.5	477.3	867.5	108.2	108.8	18.67	296.9	65.20	459.9	45.04	1649	861.3
Cell line	SW 780		UM-UC-3		293		CAKI 2		SK-OV-3		OV-CAR-3		H69AR		NCI-H69	
	mean	SD	mean	SD	mean	SD	mean	SD	mean	SD	mean	SD	mean	SD	mean	SD
rhTRAIL95-281	120	42.43	2242	1367	10000		10000		10000		93.1	8.34	10000		10000	
Ex. 5	18.68	2.37	21.29	2.10	1126	291.0	2799	371.2	5221	170.4	15.03	0.69	1251	94.05	5270	763.7
Cell line	NCI-H460		BxPC3		HepG2		HT 144		ACHN		JURKAT A3		HL60		CCRF-CEM	
	mean	SD	mean	SD	mean	SD	mean	SD	mean	SD	mean	SD	mean	SD	mean	SD
rhTRAIL95-281	5889	111.0	64.71	31.81	10000		1734	218.5	10000		10000		10000		10000	
Ex. 5	22.95	2.57	17.6	0.85	1174	58.69	26.85	2.94	187.3	45.61	372.2	225.1	7000		7000	

2. Antitumour effectiveness of fusion proteins *in vivo* on xenografts

Antitumour activity of protein preparations was tested in a mouse model of human colon cancer HCT116

Cells

- 5 The HCT116 cells were maintained in RPMI 1640 medium (Hyclone, Logan, UT, USA) mixed in the ratio of 1:1 with Opti-MEM ((Invitrogen, Cat.22600-134) supplemented with 10% fetal calf serum and 2 mM glutamine. On the day of mice grafting, the cells were detached from the support by washing the cells with trypsin (Invitrogen), then the cells were centrifuged at 1300 rpm, 4°C, 8 min.,
10 suspended in HBSS buffer (Hanks medium), counted and diluted to the concentration of 25×10^6 cells/ml.

- The PLC/PRF/5 (CLS) cells were maintained in DMEM (HyClone, Logan, UT, USA) supplemented with 10% fetal calf serum and 2 mM glutamine. On the day of mice grafting, the cells were detached from the support by washing the cells with
15 trypsin (Invitrogen), then the cells were centrifuged at 1300 rpm, 4°C, 8 min., suspended in HBSS buffer (Hanks medium), counted and diluted to the concentration of 25×10^6 cells/ml.

- The HepG2cells were maintained in MEM (HyClone, Logan, UT, USA) supplemented with 10% fetal calf serum and 2 mM glutamine. On the day of mice grafting, the
20 cells were detached from the support by washing the cells with trypsin (Invitrogen), then the cells were centrifuged at 1300 rpm, 4°C, 8 min., suspended in HBSS buffer (Hanks medium), counted and diluted to the concentration of 25×10^6 cells/ml.

Mice

- 25 Examination of antitumor activity of proteins of the invention was conducted on 7-9 week-old CD- nude (Crl:CD1-*Foxn1*^{nu} 1) or on 4-5 week old Crl:SHO-Prkdc^{scid}Hr^{hr} mice obtained from Charles River Germany. Mice were kept under specific pathogen-free conditions with free access to food and demineralised water (*ad libitum*). All experiments on animals were carried in accordance with the
30 guidelines: "Interdisciplinary Principles and Guidelines for the Use of Animals in Research, Marketing and Education" issued by the New York Academy of Sciences' Ad Hoc Committee on Animal Research and were approved by the IV Local Ethics Committee on Animal Experimentation in Warsaw (No. 71/2009).

The course and evaluation of the experimentsHuman colon cancer modelmice Crl:CD1-Foxn1^{nu} 1

On day 0 mice Crl:CD1-Foxn1^{nu} 1 were grafted subcutaneously (sc) in the right
5 side with 5×10^6 of HCT116 cells suspended in 0.2 ml HBSS buffer by means of a
syringe with a 0.5 x25 mm needle (Bogmark). When tumors reached the size of
~ 50-140 mm³ (day 14), mice were randomized to obtain the average size of
tumors in the group of ~ 70 mm³ and assigned to treatment groups. The
treatment groups were administered with the preparations of fusion proteins of
10 the invention of Ex. 3, Ex. 12 and Ex.14 (10 mg/kg), and rhTRAIL114-281 (10
mg/kg) as a comparative reference and formulation buffer (5 mM NaH₂PO₄, 95
mM Na₂HPO₄, 200 mM NaCl, 5 mM glutathione, 0,1 mM ZnCl₂, 10% glycerol, 80
mM saccharose, pH 8,0) as a control. The preparations were administered
intravenously (*i.v.*) daily for ten days on days 8-12 and 15-19. When a
15 therapeutic group reached the average tumor size of ~ 1000 mm³, mice were
sacrificed by disruption of the spinal cord. The control group received
rhTRAIL114-281.

mice Crl:SHO-Prkdc^{scid}Hr^{hr}

On day 0 mice Crl:SHO-Prkdc^{scid}Hr^{hr} were grafted subcutaneously (sc) in the right
20 side with 5×10^6 of HCT116 cells suspended in 0.1 ml HBSS buffer by means of a
syringe with a 0.5 x25 mm needle (Bogmark). When tumors reached the size of
200- 700 mm³ (day 18), mice were randomized to obtain the average size of
tumors in the group of ~ 400 mm³ and assigned to treatment groups. The
treatment groups were administered with the preparations of fusion proteins of
25 the invention of Ex. 14 (50 mg/kg), rhTRAIL114-281 (20 mg/kg) as a comparative
reference and formulation buffer (5 mM NaH₂PO₄, 95 mM Na₂HPO₄, 200 mM NaCl,
5 mM glutathione, 0,1 mM ZnCl₂, 10% glycerol, 80 mM saccharose, pH 8,0) as a
control. The preparations were administered intravenously (*i.v.*) 6 times every
second day. On the 32nd day of the experiment the mice were sacrificed by
30 disruption of the spinal cord.

Human liver cancer model

PLC/PRF/5 cells

On day 0 mice Crl:SHO-Prkdc^{scid}Hr^{hr} were grafted subcutaneously (sc) in the right side with 7×10^6 of PLC/PRF/5 cells suspended in 0.1 ml mixture of HBSS:MatrigelTM (3:1) buffer by means of a syringe with a 0.5 x25 mm needle (Bogmark). When tumors reached the size of 140 - 300 mm³ (day 31), mice were randomized to obtain the average size of tumors in the group of ~ 200 mm³ and assigned to treatment groups. The treatment groups were administered with the preparations of fusion proteins of the invention of Ex. 14 (20 mg/kg), rhTRAIL114-281 (30 mg/kg) as a comparative reference, and formulation buffer (5 mM NaH₂PO₄, 95 mM Na₂HPO₄, 200 mM NaCl, 5 mM glutathione, 0,1 mM ZnCl₂, 10% glycerol, 80 mM saccharose, pH 8,0) as a control. The preparations were administered intravenously (i.v.) 4 times every third day and subsequently 2 times every second day (q3dx4 and q2dx2). On the 32nd day of the experiment the mice were sacrificed by disruption of the spinal cord.

HepG2 cells

On day 0 mice Crl:SHO-Prkdc^{scid}Hr^{hr} were grafted subcutaneously (sc) in the right side with 7×10^6 of HepG2 cells suspended in 0.1 ml mixture of HBSS:Matrigel (3:1) buffer by means of a syringe with a 0.5 x25 mm needle (Bogmark). When tumors reached the size of 250 - 390 mm³ (day 19), mice were randomized to obtain the average size of tumors in the group of ~ 330 mm³ and assigned to treatment groups. The treatment groups were administered with the preparations of fusion proteins of the invention of Ex. 14 (50 mg/kg), rhTRAIL114-281 (30 mg/kg) as a comparative reference, and against formulation buffer (5 mM NaH₂PO₄, 95 mM Na₂HPO₄, 200 mM NaCl, 5 mM glutathione, 0,1 mM ZnCl₂, 10% glycerol, 80 mM saccharose, pH 8,0) as a control. The preparations were administered intravenously (i.v.) 6 times every second day. On the 31 day of the experiment the mice were sacrificed by disruption of the spinal cord.

Tumor size was measured using an electronic calliper, tumor volume was calculated using the formula: $(a^2 \times b)/2$, where a = shorter diagonal of the 25 tumor (mm) and b = longer diagonal of the tumor (mm). Inhibition of tumor growth was calculated using the formula:

$$\text{TGI [\%]} (\text{Tumor growth inhibition}) = (\text{WT}/\text{WC}) \times 100 - 100\%$$

wherein WT refers to the average tumor volume in the treatment group, WC refers to the average tumor volume in the control group.

The experimental results are presented as a mean value $\pm$ standard deviation (SD). All calculations and graphs were prepared using the GraphPad Prism 5.0 software.

The experimental results obtained in mice Crl:CD1-*Foxn1*^{nu} burdened with HCT116 colon cancer treated with fusion proteins of the invention of Ex. 3, Ex. 12 and Ex. 14 and comparatively with rhTRAIL114-281 are shown in Fig. 6 as a diagram of changes of the tumor volume and in Figure 7 which shows tumor growth inhibition (%TGI) as the percentage of control.

The results of experiments presented in the graphs in Figures 6 and 7 show that administration of the fusion proteins of the invention of Ex. 3, Ex. 12 and Ex. 14 caused tumor HCT116 growth inhibition, with TGI respectively 71%, 67% and 75% relative to the control on 28th day of the experiment. For rhTRAIL114-281 used as the comparative reference, a slight inhibitory effect on tumor cell growth was obtained relative to the control, with TGI at the level of 44%. Thus, fusion proteins of the invention exert much stronger effect compared to TRAIL alone.

The experimental results obtained in mice Crl:SHO-Prkdc^{scid}Hr^{hr} burdened with HCT116 colon cancer treated with fusion protein of the invention of Ex. 14 20 mg/kg) and comparatively with rhTRAIL114-281 are shown in Fig. 8 as a diagram of changes of the tumor volume and in Figure 9 which shows tumor growth inhibition (%TGI) as the percentage of control.

The results of experiments presented in the graphs in Figures 8 and 9 show that administration of the fusion protein of the invention of Ex. 14 caused tumor HCT116 growth inhibition, with TGI 22,5% relative to the control on 32nd day of the experiment. For rhTRAIL114-281 used as the comparative reference, a slight inhibitory effect on tumor cell growth was obtained relative to the control, with TGI at the level of 5,6%. Thus, fusion proteins of the invention exert much stronger effect compared to TRAIL.

The experimental results obtained in mice Crl:SHO-Prkdc^{scid}Hr^{hr} burdened with PLC/PRF/5 liver cancer treated with fusion protein of the invention of Ex. 14 and

comparatively with rhTRAIL114-281 are shown in Fig. 10 as a diagram of changes of the tumor volume and in Figure 11 which shows tumor growth inhibition (%TGI) as the percentage of control.

5 The results of experiments presented in the graphs in Figures 10 and 11 show that administration of the fusion protein of the invention of Ex. 14 caused tumor PLC/PRF/5 growth inhibition, with TGI 34% relative to the control on 49th day of the experiment. For rhTRAIL114-281 used as the comparative reference, a slight inhibitory effect on tumor cell growth was obtained relative to the control, with TGI at the level of 18%. Thus, fusion proteins of the invention exert much
10 stronger effect compared to TRAIL.

The experimental results obtained in mice Crl:SHO-Prkdc^{scid}Hr^{hr} burdened with HepG2 liver cancer treated with fusion protein of the invention of Ex. 14 and comparatively with rhTRAIL114-281 are shown in Fig. 12 as a diagram of changes of the tumor volume and in Figure 13 which shows tumor growth inhibition
15 (%TGI) as the percentage of control.

The results of experiments presented in the graphs in Figures 12 and 13 show that administration of the fusion protein of the invention of Ex. 14 caused tumor HepG2 growth inhibition, with TGI 33.6% relative to the control on 31 day of the experiment. For rhTRAIL114-281 used as the reference preparation, a slight
20 inhibitory effect on tumor cell growth was obtained relative to the control, with TGI at the level of 7%. Thus, fusion proteins of the invention exert much stronger effect compared to TRAIL.

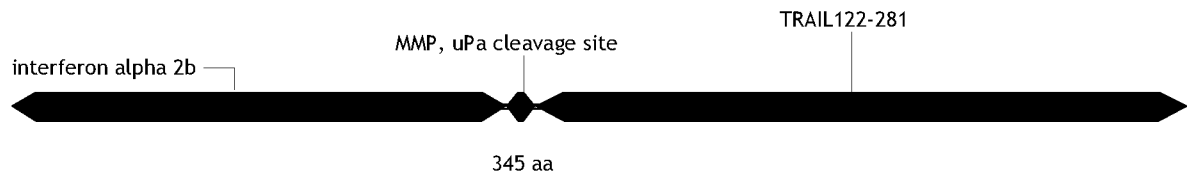
The tested fusion proteins did not cause significant side effects manifested by a decrease in body weight of mice (i.e. less than 10% of the baseline body weight).
25 This shows low systemic toxicity of the protein.

Claims

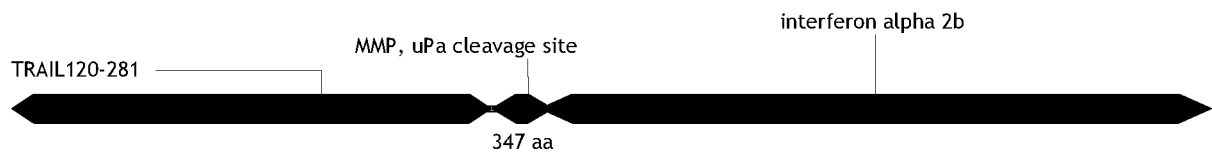
1. A fusion protein comprising:
- domain (a) which is a functional fragment of hTRAIL protein sequence, which fragment begins with an amino acid at a position from the range hTRAIL95 to hTRAIL122, inclusive, and ends with the amino acid hTRAIL281, or a homolog of said functional fragment having at least 70% sequence identity, wherein said functional fragment or homolog thereof binds to receptors on the surface of mammalian cells and induces an apoptotic signal in the cells, and wherein hTRAIL protein has the amino acid sequence set forth as SEQ. No. 16; and
- domain (b) which is a sequence of an immunostimulating effector peptide,
- selected from the group consisting of
- the pseudodimer of interferon gamma with an amino acid sequence consisting of SEQ. No. 19, and
 - the pseudodimer of interferon alpha 2b with an amino acid sequence consisting of SEQ. No. 46;
- wherein the sequence of domain (b) is attached at the C-terminus or N-terminus of domain (a).
2. The fusion protein according to claim 1, wherein domain (a) is selected from the group consisting of fragments of hTRAIL beginning with an amino acid in position 95, 114, 116, 120, 121 or 122.
3. The fusion protein according to claim 1 or 2, which between domain (a) and domain (b) contains at least one domain (c) comprising a protease cleavage site selected from the group consisting of a sequence recognized by metalloprotease MMP, sequence recognized by urokinase uPA, and combinations thereof.
4. The fusion protein according to claim 3, wherein the sequence recognized by metalloprotease MMP is SEQ. No. 20, and the sequence recognized by urokinase uPA is SEQ. No. 21.

5. The fusion protein according to claim 3 or 4, wherein domain (c) is a combination of the sequence recognized by metalloprotease MMP and the sequence recognized by urokinase uPA located next to each other.
- 5 6. The fusion protein according to any one of claims 3 to 5, which comprises two domains (c), and wherein between said two domains (c) there is a domain (d) of a linker for attachment of a PEG molecule with an amino acid sequence selected from the group consisting of SEQ. No. 22, SEQ. No. 23, SEQ. No. 24 and SEQ. No. 25.
- 10 7. The fusion protein according to any one of claims 3 to 6 which additionally comprises a glycine-serine flexible steric linker between domains (a), (b), (c) or (d).
8. The fusion protein according to claim 7, wherein the glycine-serine linker has an amino acid sequence selected from the group consisting of SEQ. No. 26, SEQ. No. 27, SEQ. No. 28, and SEQ. No. 50.
- 15 9. The fusion protein according to claim 1 the amino acid sequence of which is selected from the group consisting of SEQ. No. 12; SEQ. No. 13; SEQ. No. 14; SEQ. No. 15; and SEQ. No. 44.
10. The fusion protein according to any one of claims 1 to 9, which is a recombinant protein.
- 20 11. A polynucleotide, encoding the fusion protein defined as in any one of claims 1 to 9.
12. The polynucleotide according to claim 11, with a nucleotide sequence selected from the group consisting of SEQ. No. 41; SEQ. No. 42; SEQ. No. 43; and SEQ. No. 48.
- 25 13. An expression vector, comprising the polynucleotide sequence according to claim 11 or 12.
14. A host cell, comprising the expression vector as defined in claim 13.

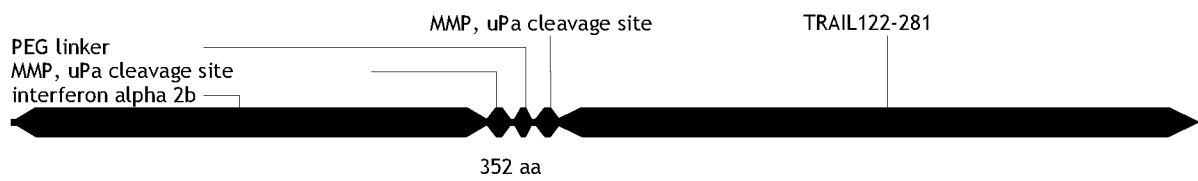
15. The host cell according to claim 14, which is an E. coli cell.
16. A pharmaceutical composition, comprising the fusion protein as defined in any one of claims 1 to 10 in combination with a pharmaceutically acceptable carrier.
- 5 17. The pharmaceutical composition as defined in claim 16 in a form for parenteral administration.
18. Use of the fusion protein as defined in any one of claims 1 to 10 for the treatment of cancer in mammals.
19. The use of claim 18, wherein the mammal is a human.



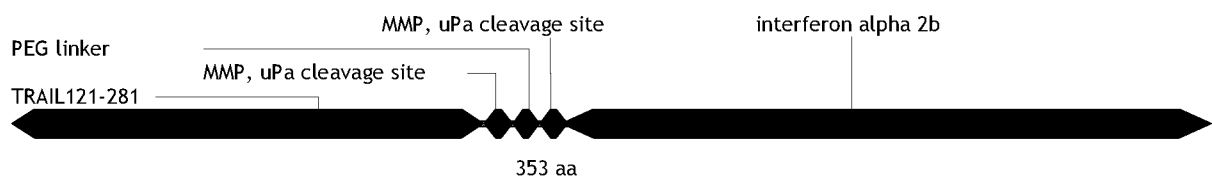
Ex. 1



Ex.2



Ex. 3



Ex.4

Fig. 1

2/9

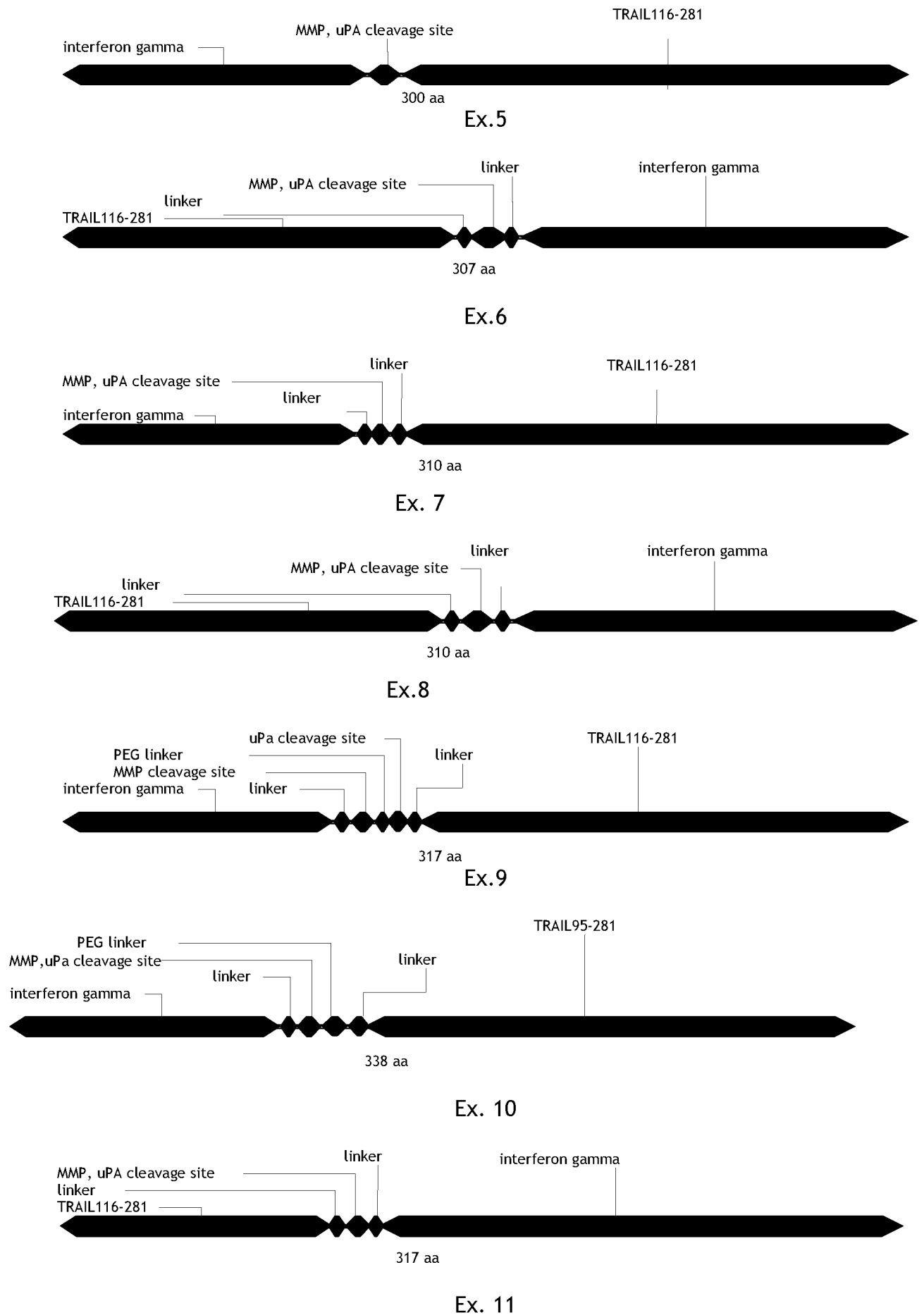
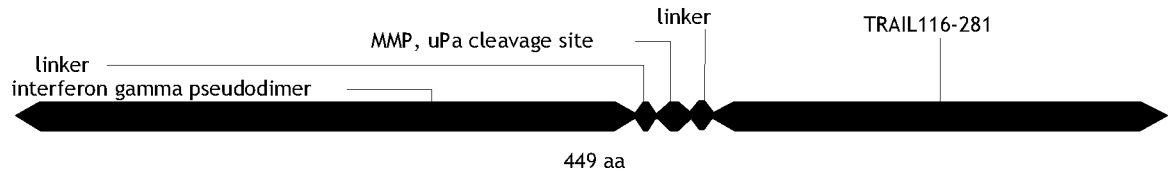
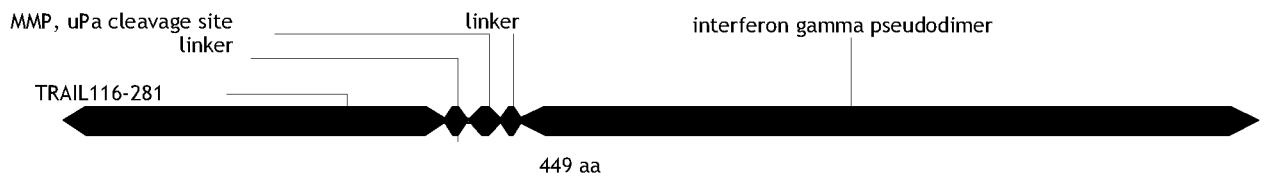


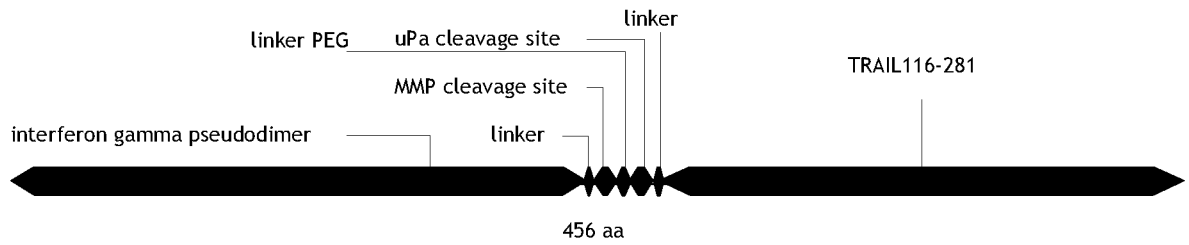
Fig. 2



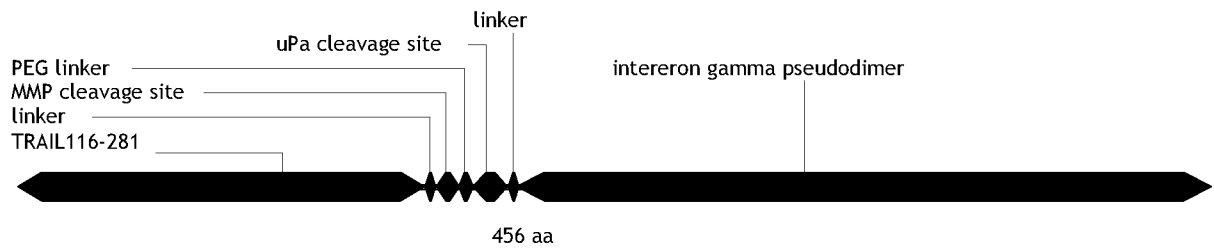
Ex. 12



Ex.13



Ex.14



Ex.15

Fig. 3

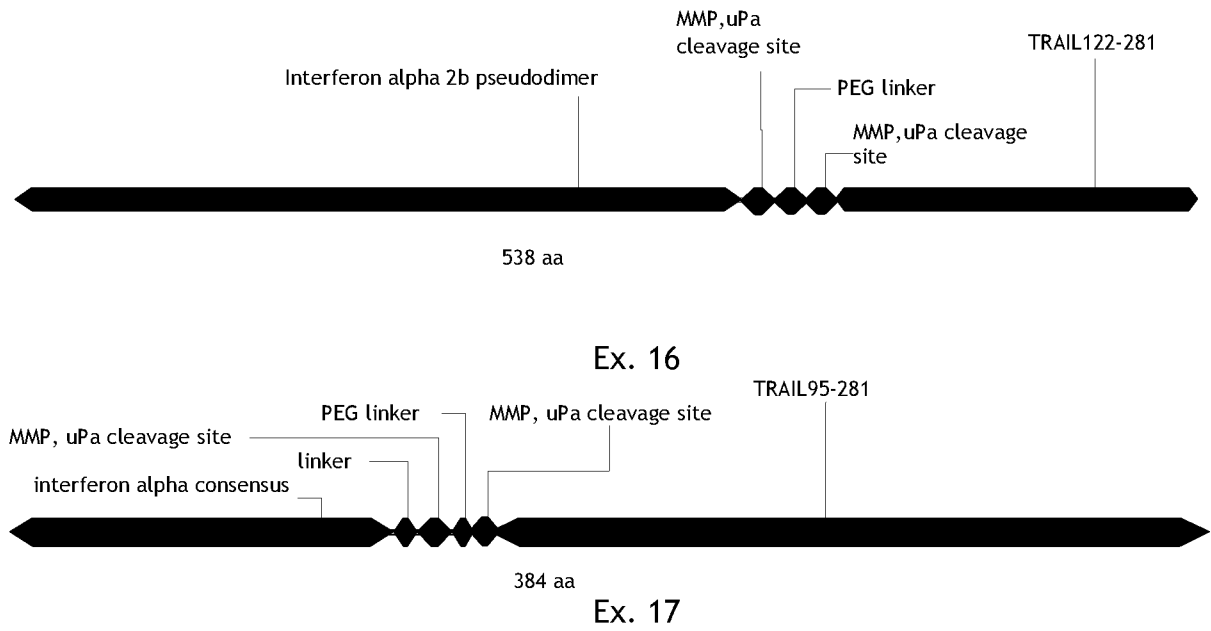
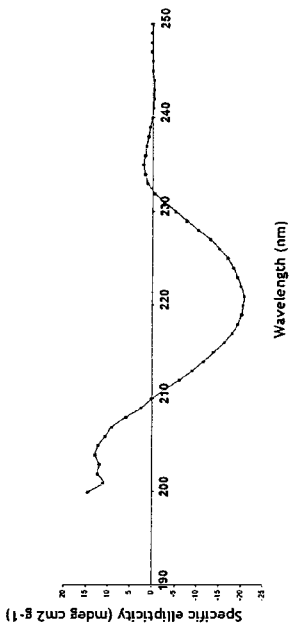
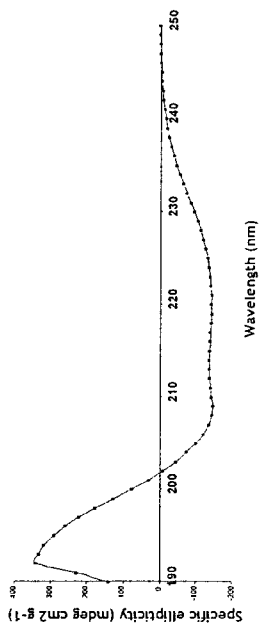


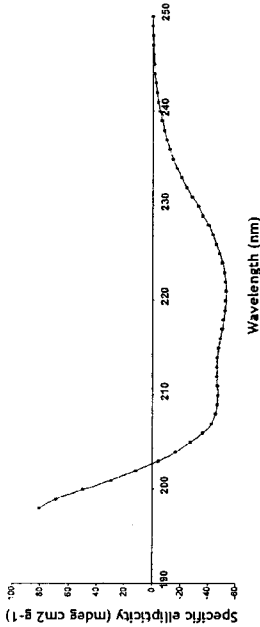
Fig. 4



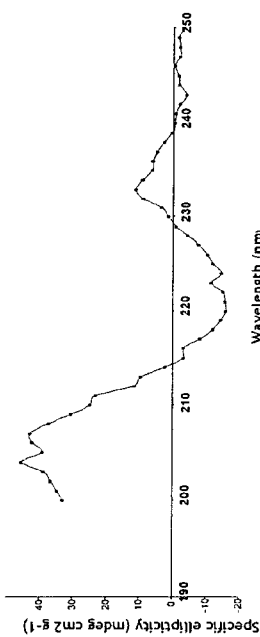
rhTRAIL95-281 protein



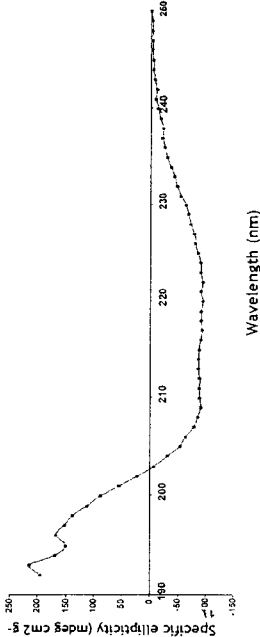
Ex. 5



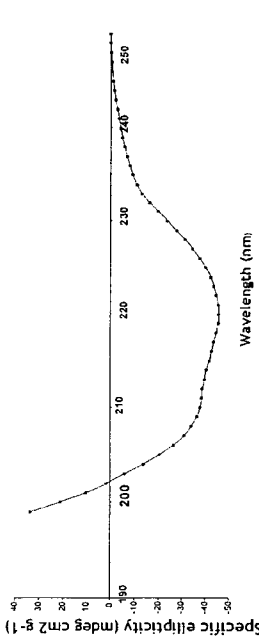
Ex. 14



rhTRAIL114-281 protein



Ex. 12



Ex. 3

Fig. 5

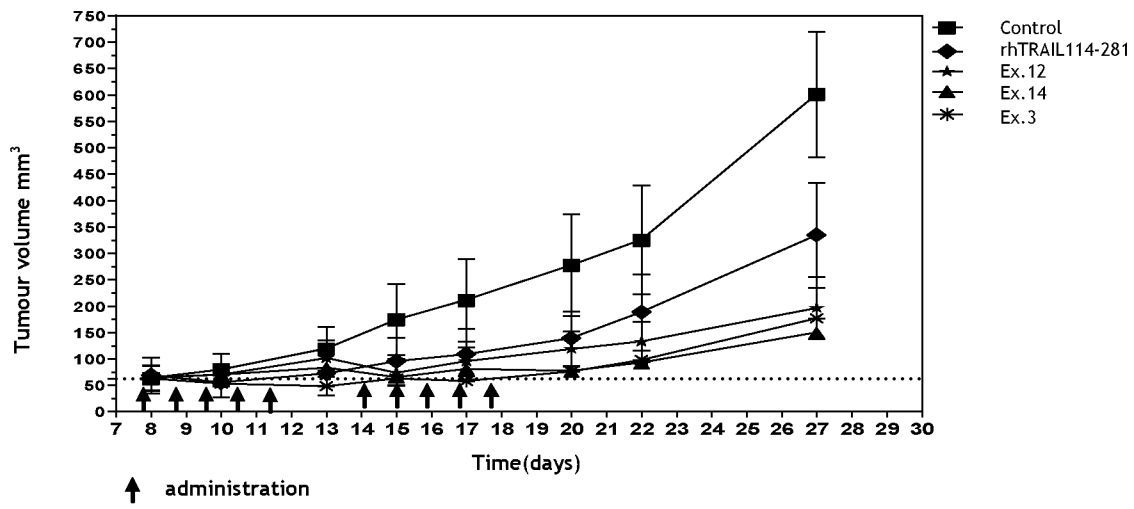


Fig. 6

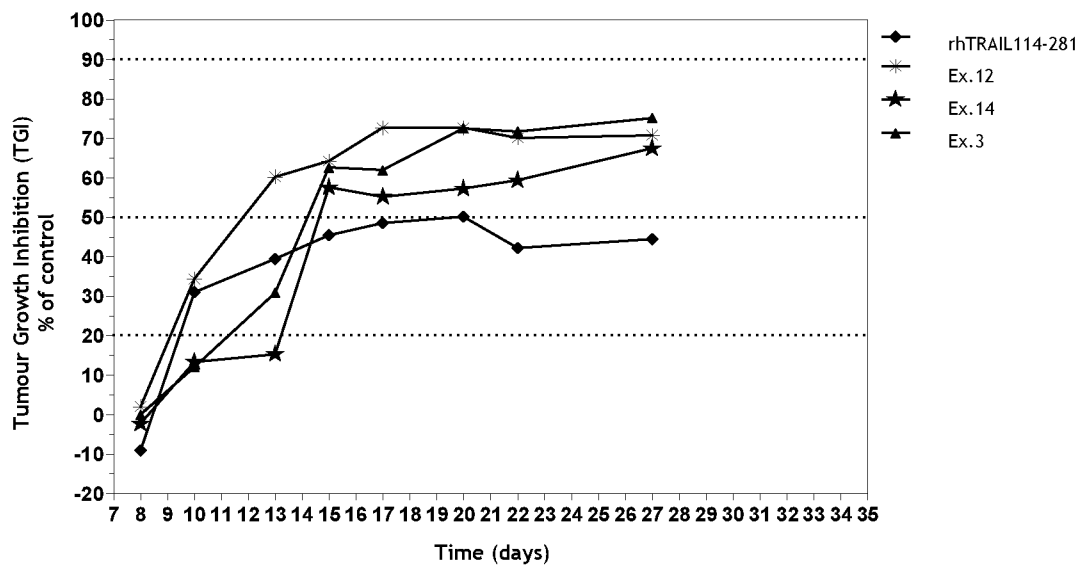


Fig. 7

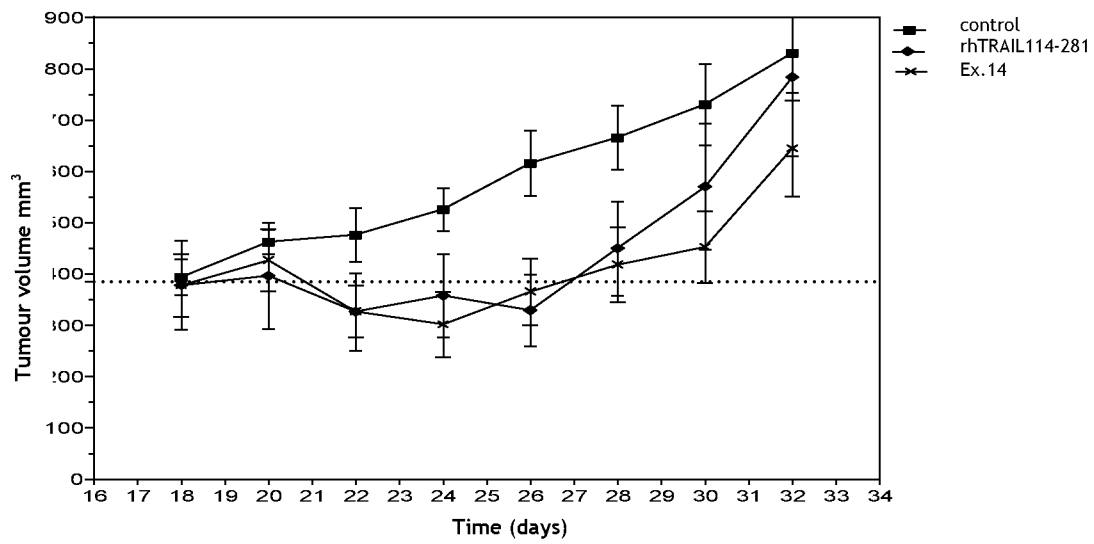


Fig. 8

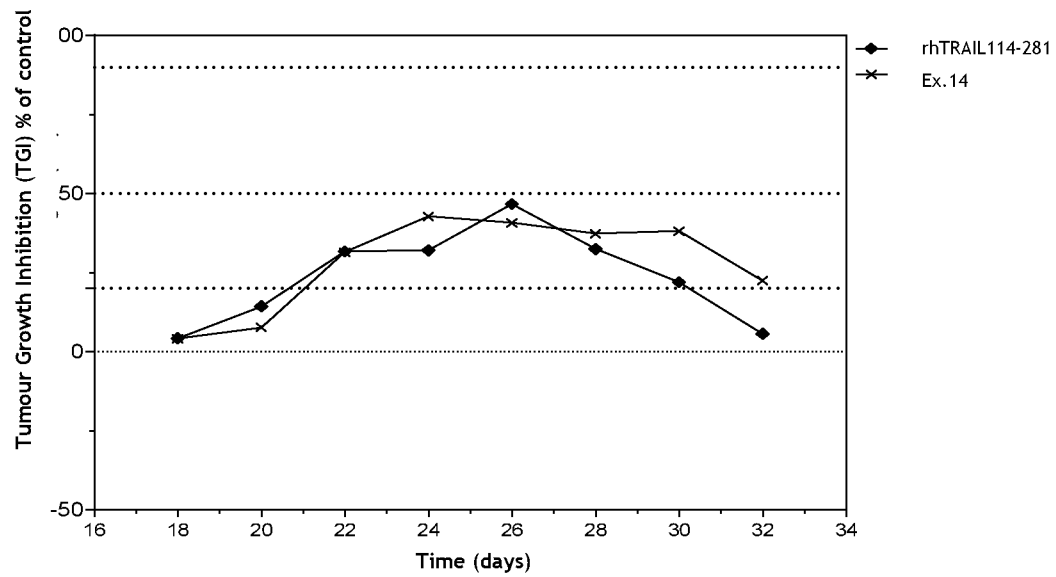


Fig.9

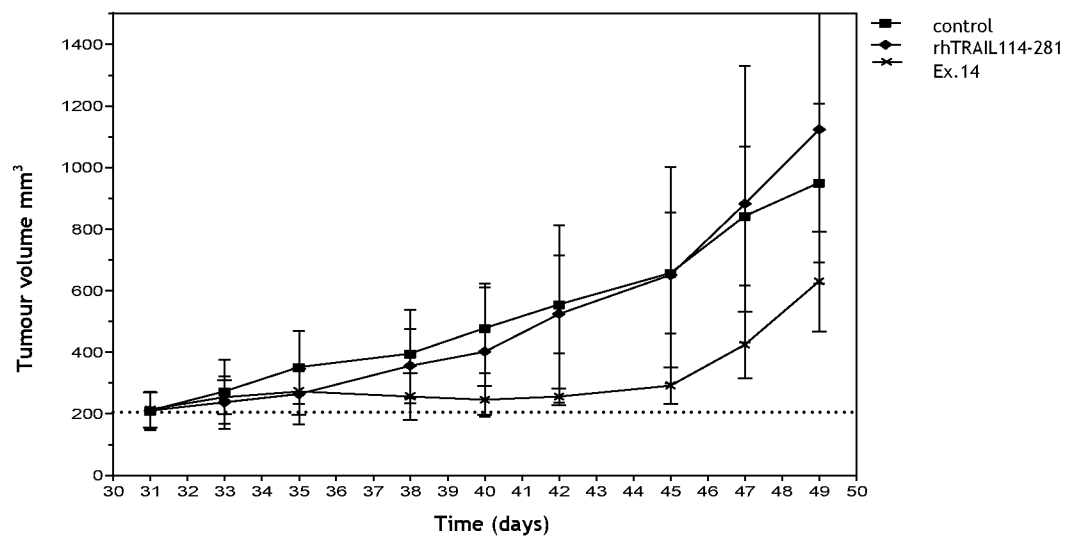


Fig. 10

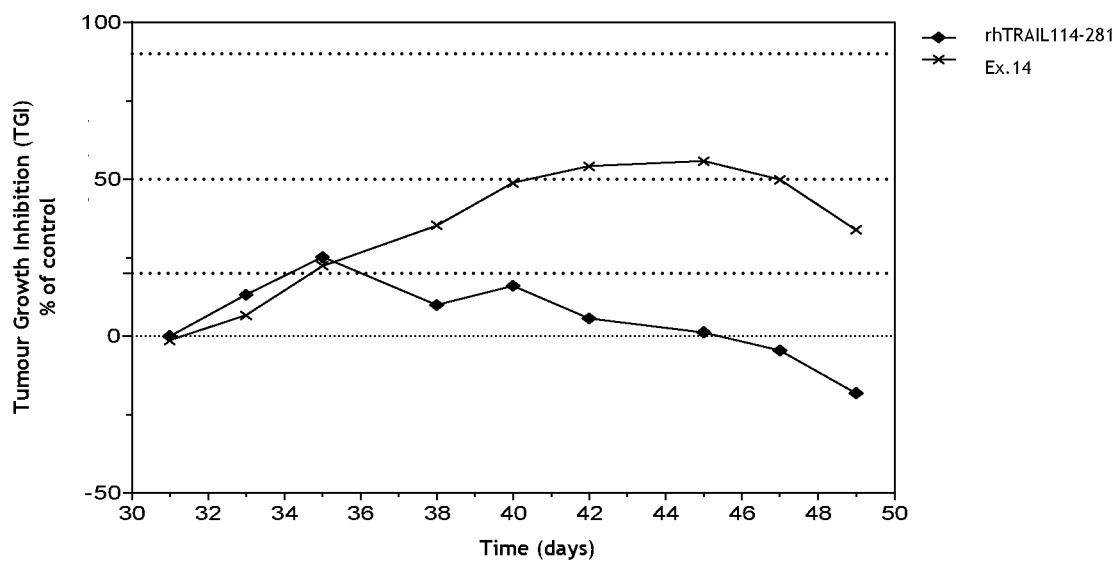


Fig.11

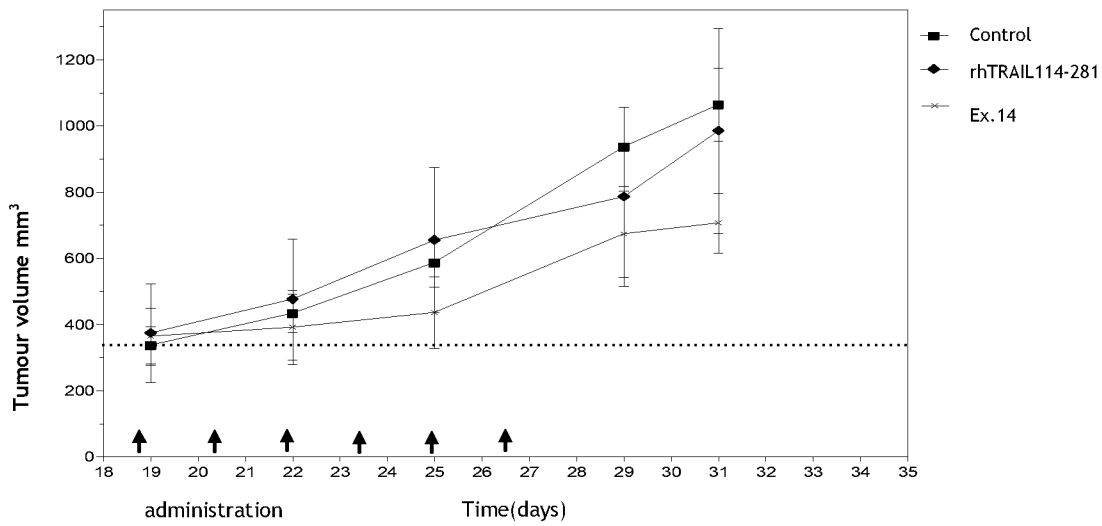


Fig. 12

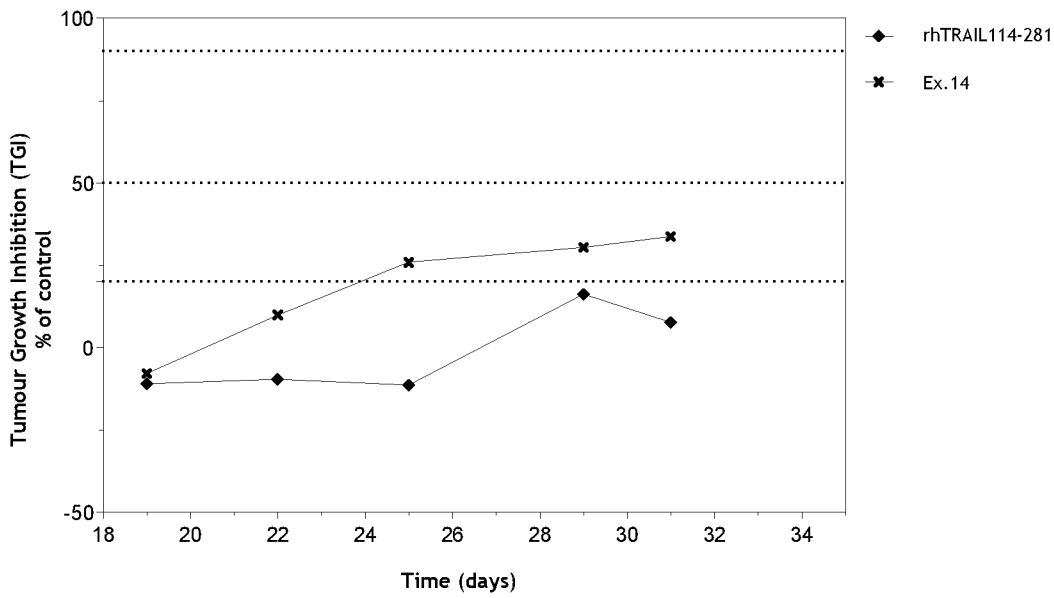


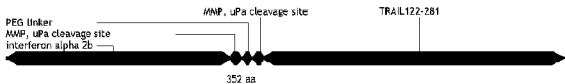
Fig. 13



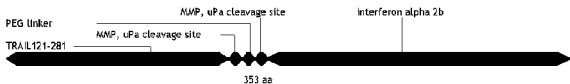
Ex. 1



Ex. 2



Ex. 3



Ex. 4